

FIG.1



GGC ACC GGG GCG CCG CCG CCG CTG CTG CTA CTG CCG CTG CTG CTG CTC CTA GGG ACC GGC
Gly Thr Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr Gly

CTC TTG CCT GCT AGC AGC CAC ATA GAG ACC CGG GCC CAT GCG GAG GAG CGG CTC CTG AAG
Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys

AGA CTC TTC TCC GGT TAC AAC AAG TGG TCT CGG CCA GTA GGC AAT ATC TCA GAT GTG GTC
Arg Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val

CTC GTC CCG TTT GGC TTG TCC ATT GCT CAG CTC ATT GAC GTG GAC GAG AAG AAC CAG ATG
Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met

ATG ACA ACC AAC GTG TGG GTG AAG CAG GAG TGG CAC GAC TAC AAG CTG CCG TGG GAC CCT
Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp Pro

GGT GAC TAC GAG AAT GTC ACC TCC ATC CCG ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC
Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp

ATC GTC CTC TAC AAC AAT GCG GAT GGA GAC TTT GCA GTC ACC CAC CTC ACC AAG GCC CAC
Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His

CTG TTC TAT GAC GGA AGG GTG CAG TGG ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC
Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser

ATC GAC GTC ACC TTC TTC CCG TTT GAC CAG CAG AAC TGT ACC ATG AAG TTT GGA TCC TGG
Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Gly Ser Trp

ACC TAC GAC AAG GCC AAG ATT GAC TTA GTG AGC ATT CAT AGC CGT GTG GAC CAA CTG GAC
Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp

TTC TGG GAA AGT GGG GAG TGG GTC ATC GTG GAT GCT GTG GGC ACC TAC AAC ACC AGG AAG
Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys

TAC GAG TGC TGT GCC GAG ATC TAT CCT GAC ATC ACC TAT GCC TTC ATC ATC CGA CCG CTG
Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile The Tyr Ala Phe Ile Ile Arg Arg Leu

CCG CTA TTC TAC ACC ATC AAC CTC ATC ATC CCG TGC CTG CTC ATC TCC TGT CTC ACC GTG
Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val

FIG. 2A-1



790 810 830
CTG GTC TTC TAT CTG CCT TCA GAG TGT GGC GAG AAG GTC ACA CTG TGC ATC TCG GTG CTG
Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu

850 870 890
CTT TCT CTC ACC GTC TTC CTG CTG CTC ATC ACC GAG ATC ATC CCG TCC ACC TCG CTG GTG
Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val

910 930 950
ATC CCG CTC ATC GGC GAG TAC CTC CTC TTC ACC ATG ATC TTC GTC ACC CTC TCC ATC GTG
Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val

970 990 1010
ATC ACG GTC TTC GTG CTC AAT GTG CAC CAC CGC TCG CCA CGC ACA CAC ACG ATG CCC GCC
Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro Ala

1030 1050 1070
TGG GTG CGT AGA GTC TTC CTG GAC ATC GTG CCT CGC CTC CTC TTC ATG AAG CGC CCC TCT
Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser

1090 1110 1130
GTG GTC AAA GAC AAC TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC CCC
Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro

1150 1170 1190
CGC TTC TGG CCA GAG CCT GTG GGC GAG CCC GGC ATC TTG AGT GAC ATC TGC AAC CAA GGT
Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly

1210 1230 1250
CTG TCA CCT GCC CCA ACT TTC TGC AAC CCC ACG GAC ACA GCA GTC GAG ACC CAG CCT ACG
Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr

1270 1290 1310
TGC AGG TCA CCC CCC CTT GAG GTC CCT GAC TTG AAG ACA TCA GAG GTT GAG AAG GCC AGT
Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser

1330 1350 1370
CCC TGT CCA TCG CCT GGC TCC TGT CCT CCA CCC AAG AGC AGC AGT GGG GCT CCA ATG CTC
Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu

1390 1410 1430
ATC AAA GCC AGG TCC CTG AGT GTC CAG CAT GTG CCC AGC TCC CAA GAA GCA GCA GAA GAT
Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Asp

1450 1470 1490
GGC ATC CGC TGC CGG TCT CGG AGT ATC CAG TAC TGT GTT TCC CAA GAT GGA GCT GCC TCC
Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser

1510 1530 1550
CTG GCT GAC AGC AAG CCC ACC AGC TCC CCG ACC TCC CTG AAG GCC CGT CCA TCC CAG CTT
Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu

FIG.2A-2



1570 1590 1610
CCC GTG TCA GAC CAG GCC TCT CCA TGC AAA TGC ACA TGC AAG GAA CCA TCT CCT GTG TCC
Pro Val Ser Asp Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser

1630 1650 1670
CCA GTC ACT GTG CAC AAG GCG GGA GGC ACC AAA GCA CCT CCC CAA CAC CTG CCC CTG TCA
Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu Pro Leu Ser

1690 1710 1730
CCA GCC CTG ACA CGG GCA GTA GAA GGC GTC CAG TAC ATT GCA GAC CAC CTC AAG GCA GAA
Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu Lys Ala Glu

1750 1770 1790
GAC ACT GAC TTC TCG GTG AAG GAG GAC TGG AAA TAC GTG GCC ATG GTC ATT GAC CGA ATC
Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile

1810 1830 1850
TTC CTC TGG ATG TTC ATC ATT GTC TGC CTT CTG GGC ACT GTG GGA CTC TTC CTG CCT CCC
Phe Leu Trp Met Phe Ile Ile Val Cys Leu Lue Gly Thr Val Gly Leu Phe Leu Pro Pro

1870 1890 1917
TGG CTG GCT GCT TGC TGA TGGCTTCGACAGTGTCTCAGGCTCACGTCTCCTGCTGACTTTGTTTCCAG
Trp Leu Ala Ala Cys

1943 1969 1997
TTTCTTCTCCGACAAAGTTGGCCTCCCTTCATTTATTCCTGTTATTTTGGGCTTCGTGTTATTAATATCCTTCCCTGCC
TCTGTGGCGCATTGTAAGTTTTAAAAATTAATAGACCAAAGCC...3'

4-2 cDNA: 3' end
↓
1867 1884 1912
CCC TGG CTG GCT GGT ATG ATC TAG GGACGTGGTGGTGCCAGCTCCACATCTCTGTAGGGCCATAC
Pro Trp Leu Ala Gly Met Ile

1937 1963 1991
GACTCGTCAGTCAACCCACATCTTCCAAACCGGCTGACCATGAGACACCCTAGGAGAGAGATGATGCTTCTTGGGAGATG

2016 2042 2070
GAAGTTGGCCCTGTTCTAGTCAGACTATGGGCGTGGTTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCC

2095 2121 2149
CATTAAAGTTTCTCCAGAGCAAGTGGCAGTACTCCCTGACTTACAGACAGCACACCCCATCTGTGTACAGAGAATGA

2174 2200 2228
TCCCGAGTTGATCTCAGTTGTCCTTTGAGGCCATGAAAAATTCATCCACCTTGAGGAACCCAGACCTCTCATGCTGTGG

2253 2279 2307
GATCAATAAGACCAGGAATCTCCACTGTGACTCTGCTGGCCACACCCTCTCCCTCCCCAAGAAGTGGTCCCTCATCC
CCCAATTC...3'

FIG.2A-3



ATAAGTCTCCGGCAGTTGCTTTTGACCACAGAGGGACGAGCGGCCCGCGCACGCGCGCAGTCTTCGAGCGGAGCGCGGCGACAGCCGGCAGCCGCCGCA
-210 -180 -150 -120

GCCTGTAGAGCCCGCCTCGCGTGGGCC
Met Glu Ile Gly Gly Pro Gly Ala Pro Pro Pro Leu Leu Leu Leu Leu Leu Thr
ATG GAG ATC GGG GGC CCC GCG CCG CCG CCG CTG CTG CTA CTG CCG CTG CTC CTA GGG ACC

[illegible]

Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln
 TCT CGG CCA GTA GGC AAT ATC TCA GAT GTG GTC CTC CTC GTC CGC TTT GGC TTT GGC TCC ATT GCT CAG CTC ATT GAC GTG GAC GAG AAC CAG
 30 40 50 60 70 80 90 100 110 120 130 140 150

[illegible]

Arg 116 Pro Ser Glu Leu 115 Ile Trp Arg Pro Asp Ile Val Leu Tyr 100 Asn Ala Asp Gly Asp Phe Ala Val Thr His 110
CGC ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC ATC GTC CTC TAC AAC AAT GCG GAT GGA GAC TTT GCA GTC ACC CAC CTG ACC Leu Thr Lys Ala
300 270

His Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val Thr Phe Pro Phe Asp
 CAC CTG TTC TAT GAC GGA AGG GTG CAG TGG ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC ATC GAC GTG ACC TTC CCC TTT GAC
 120 130 360 390 420 140

Gln Gln Asn Cys Thr
 CAG CAG AAC TGT ACC
 150
 Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu
 450 480
 ATG AAG TTT GGA TCC TGG ACC TAC GAC AAG GCC AAG ATT GAC TTA GTG AGC ATT CAT AGC CGT GTG GAC CAA CTG
 170 510

FIG. 2B-1



180 Asp Phe Trp Glu Ser 190 Tyr Asn Thr Arg Lys Tyr Glu Cys Cys 200 Glu Ile Tyr Pro
GAC TTC TGG GAA AGT 540 TAC AAC ACC AGG AAG TAC GAG TGC TGT 600 GCC GAG ATC TAT CCT
210 Asp Ile Thr Tyr Ala Phe 220 Ile Asn Leu Ile Ile Pro Cys Leu Leu 230 Ser Cys Leu Thr
GAC ATC ACC TAT GCC 630 ATC CGA CGC CTG CCG CTA TTC TAC 660 ACC ATC CCG TGC CTG CTC ACC 690 TCC TGT CTC ACC
240 Val Leu Val Phe Tyr 250 Cys Ile Ser Val Leu Leu Ser Leu Thr 260 Phe Leu Leu Leu
GTG CTG GTC TTC TAT 720 Pro Ser Glu Cys Gly Glu Lys Val Thr 750 Cys TGC ATC TCG GTG CTG CTT TCT CTC ACC 780 Val Phe Leu Leu Leu
270 Ile Thr Glu Ile Ile 280 Glu Tyr Leu Leu Phe Thr Met Ile Phe 290 Thr Leu Ser Ile
ATC ACC GAG ATC ATC 810 Ser Thr Ser Leu Val Ile Pro Leu Ile 840 Gly GAG TAC CTC CTC TTC ACC ATG ATC TTC 870 GTC ACC CTC TCC ATC
300 Val Ile Thr Val Phe Val 310 His Thr Met Pro Ala Trp Val Arg Arg 320 Phe Leu Asp Ile
GTC ATC ACC GAG ATC ATC 880 Leu Asn Val His His Arg Ser Pro Arg Thr 930 ACA CAC ACB ATG CCC GGC TGG GTG CGT AGA 960 GTC TTC CTG GAC ATC
330 Val Pro Arg Leu Leu 340 Cys Arg Arg Leu Ile Glu Ser Met His 350 Met Ala Asn Ala
GTG CCT CGC CTC CTC 990 Met Lys Arg Pro Ser Val Val Lys Asp Asn 1020 TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC
360 Pro Arg Phe Trp Pro Glu 370 Ile Cys Asn Gln Gly Leu Ser Pro Ala 380 Thr Phe Cys Asn
CCC CGC TTC TGG CCA 1080 CCT GTG GGC GAG CCC GGC ATC TTG AGT 1110 GAC ATC TGC AAC CAA GGT CTG TCA CCT GCC CCA ACT TTC TGC AAC
390 Pro Thr Asp Thr Ala Val 400 Leu Glu Val Pro Asp Leu Lys Thr Ser 410 Val Glu Lys Ala
CCC ACG GAC ACA GCA 1170 Glu Thr Gln Pro Thr Cys Arg Ser Pro Pro 1230 GAG GTC CCT GAC TTG AAG ACA TCA GAG GTT GAG AAG GCC

FIG.2B-2

[illegible]

FIG. 2B-3

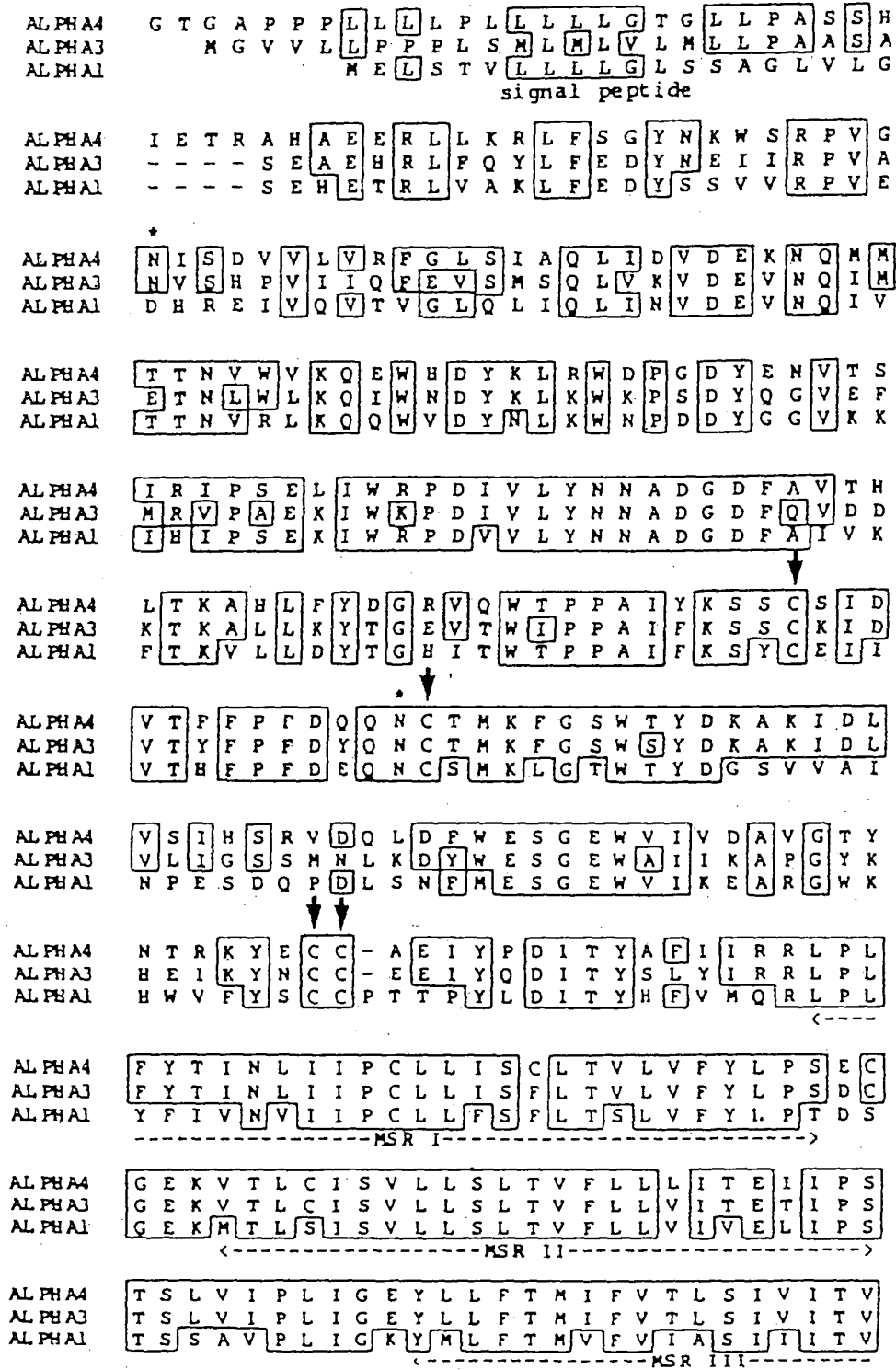


FIG.3A



ALPHA4 F V L N V H H R S P R T H T M P A W V R R V F L D I V
ALPHA3 F V L N V H Y R T P T T H T M P T W V K A V F L N L L
ALPHA1 I V I N T H H R S P S T H I M P E W V R K V F I D T I
----->

ALPHA4 P R L L F - - - M K R P S V V K D N C R R L I E S M H
ALPHA3 P R V M F - - - M T R P T S G E G D T P K T - - - -
ALPHA1 P N I M F F S T M K R P S R D K Q E K R I F - - - -

ALPHA4 X M A N A P R F W P E P V G E P G I L S D I C N Q G L
ALPHA3 - - - - - - - - - - - R T F Y G A E L S N L N C F S R
ALPHA1 - - - - - - - - - - - T E D I D I S D I S G K P G

ALPHA4 S P A P T F C N P T D T A V E T Q P T C R S P P L E V
ALPHA3 A D S K S C K E G Y P C Q D G T C G Y C H H R R V K I
ALPHA1 P P P M G F H - - - - - - - - - - - - - - - - - -

ALPHA4 P D L K T S E V E K A S P C P S P G S C P P P K S S S
ALPHA3 S N F - - - - - - - - - - - - - - - - - S A N L T R S S S
ALPHA1 -

ALPHA4 G A P M L I K A R S L S V Q H V P S S Q E A A E D G I
ALPHA3 S E S V -
ALPHA1 -

ALPHA4 R C R S R S I Q Y C V S Q D G A A S L A D S K P T S S
ALPHA3 -
ALPHA1 -

ALPHA4 P T S L K A R P S Q L P V S D Q A S P C K C T C K E P
ALPHA3 -
ALPHA1 -

ALPHA4 S P V S P V T V L K A G G T K A P P Q H L P L S P A L
ALPHA3 - - - - - - - - - - - N A V L S L S A L S P E I
ALPHA1 - - - - - - - - - - - - - - - S P L I K H P E V
-----<

ALPHA4 T R A V E G V Q Y I A D H L K A E D T D F S V K E D W
ALPHA3 K E A I Q S V K Y I A E N M K A Q N V A K E I Q D D W
ALPHA1 K S A I E G V K Y I A E T M K S D Q E S N N A A E E W
amphipathic helix----->

ALPHA4 K Y V A M V I D R I F L W M F I I V C L L G T V G L F
ALPHA3 K Y V A M V I D R I F L W V F I L V C I L G T A G L F
ALPHA1 K Y V A M V M D H I L L L G V F M L V C L I G T L A V F
-----<-----MSR IV----->

ALPHA4 L P P W L A G M I
ALPHA3 L Q P L M A - R D D T
ALPHA1 A G R L I E L H Q Q G
-->

FIG.3B

FIG.4A

Clone 4-1;
Antisense

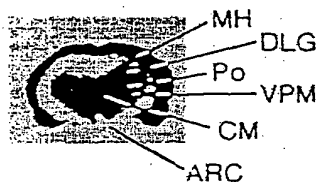
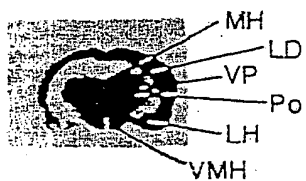
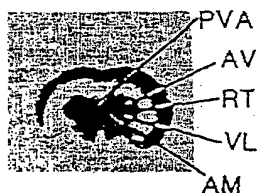


FIG.4B

Clone 4-1;
Sense

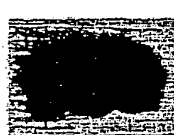
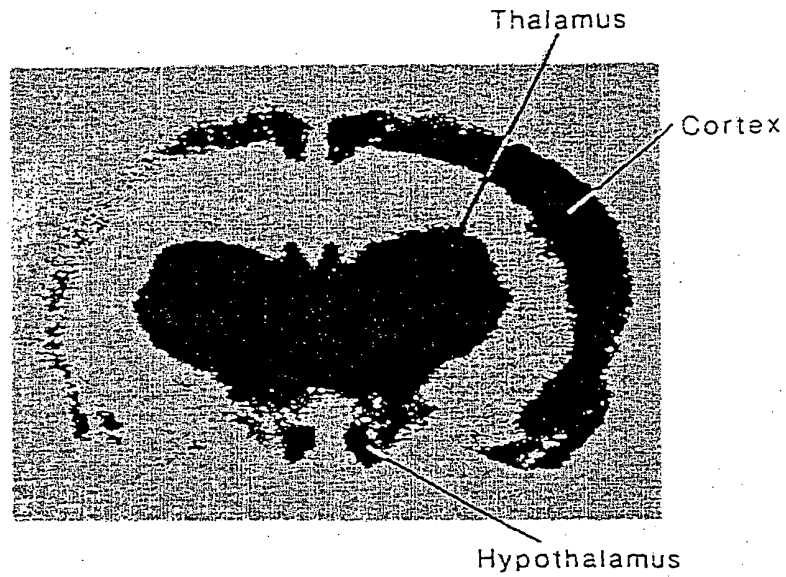
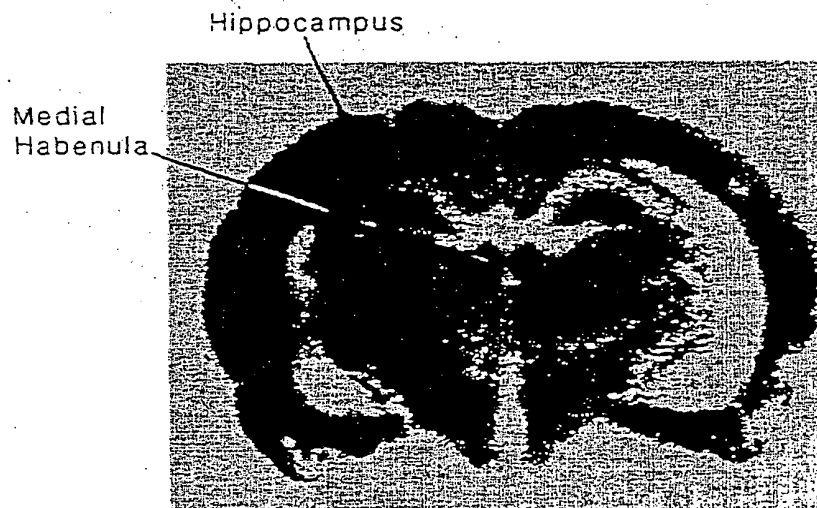


FIG.5A



PROBE: Alpha 4

FIG.5B



PROBE: Alpha 3

FIG.6A

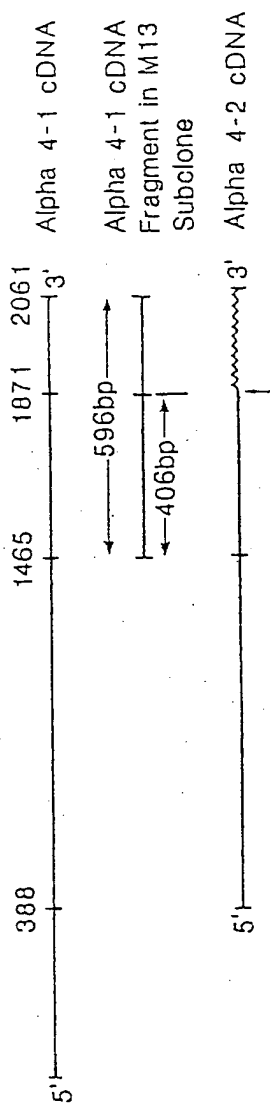


FIG.6B

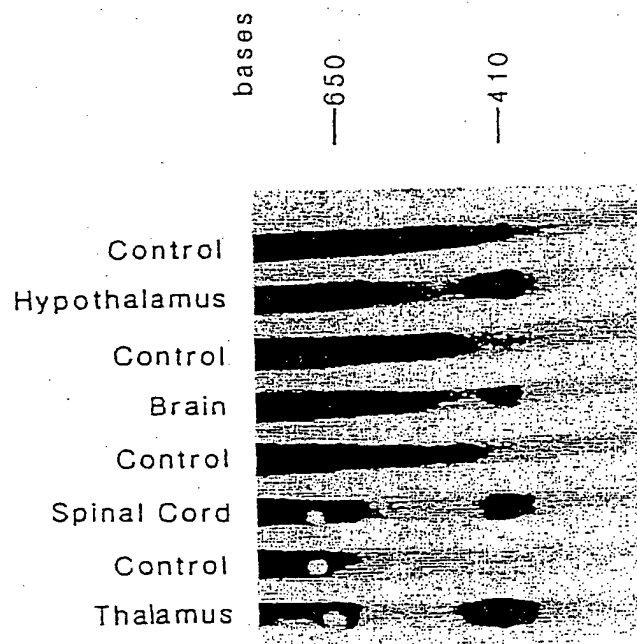
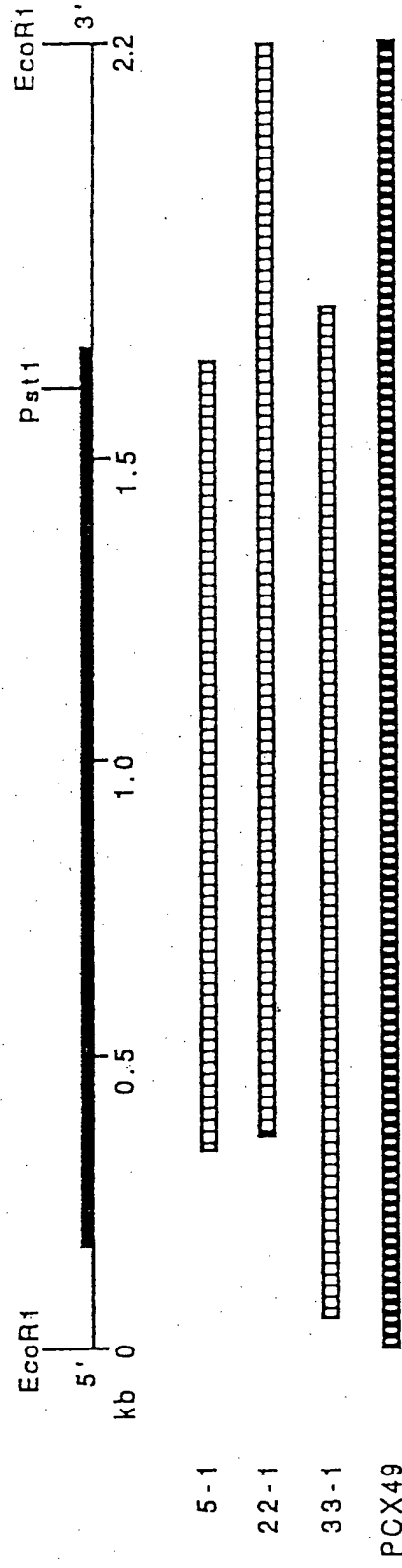




FIG.7A





5' -179 -100
TGGAGGCGGAGCCACCCGGGAGCGGGCTTCCGACCGGACCTCCCTCGTTGCAGGAAGTCCCGGTTTCAGTGAGCACCTTTAGACC
Met Leu Ala Cys Met Ala Gly His Ser Asn Ser Met Ala Leu Phe Ser Phe Ser Leu Leu Trp Leu Cys Ser Gly
ATG CTG GCT TGC ATG GCC GGG CAC TCC AAC TCA ATG GCG CTG TTC AGC CTT CTT TGG CTG TGC TCA GGG
GTT TTG GGA ACT GAC ACA GAG GAG CTA GTG GAG CAT CTC TTA GAT CCC TCC CGC TAT AAC AAG CTG ATT CGT
Val Leu Gly Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg
CCA GCT ACT AAC GGC TCT GAG CTG GTG ACT GTA CAG CTC ATG GTA TCA TTG GCT CAG CTC ATT AGT GTG CAC GAG
Pro Ala Thr Asn Gly Ser Glu Leu Val Thr Val Glu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu
CGG GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT TAC CGC CTC ACA TGG AAG CCT GAG
Arg Glu Gln Ile Met Thr Thr Asn Val Thr Leu Thr Gln Glu Trp Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro Glu
GAC TTC GAC AAT ATG AAG AAA GTC CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTT CTA TAC AAC AAT
Asp Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn Asn
GCT GAC GGC ATG TAC GAA GTC TCC TTC TAT TCC AAT GCT GTG GTC TCC TAT GAT GGC AGC ATC TTT TGG CTA CCA
Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro
CCT GCC ATC TAC AAG AGT GCA TGC AAG ATT GAG GTG AAG CAC TTC CCA TTT GAC CAG CAG AAT TGC ACC ATG AAG
Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys

FIG.7B-1

TTTT Phe 176	CGC Arg	TCA Ser	TGG Trp	ACC Thr	TAC Tyr	GAC Asp	CGT Arg	ACT Thr	GAG Glu	GAG Ile	ATT Ile	GAC Asp	CTG Leu	CTG Val	CTC Leu	570	AAA Lys	AGT Ser	GAT Asp	GTG Val	GCC Ala	AGT Ser	CTG Leu	GAT Asp	GAC Asp	TTC Phe	600
ACACA Thr 201	CCC Pro	AGC Ser	GGG Gly	GAG Glu	TGG Trp	GAC Asp	ATC Ile	ATC Ile	GCA Ala	CTG Leu	CTG Pro	CCA Pro	GGC Gly	CGA Arg	CGC Arg	630	AAC Asn	GAG Glu	AAC Asn	CCA Pro	GAC Asp	TCC Ser	ACC Thr	ACC Thr	IAT Tyr	GTG Val	
GAC Asp 226	ATC Ile	ACC Thr	TAT Tyr	GAC Asp	TTC Phe	ATC Ile	ATT Ile	CGT Arg	CGC Arg	AAA Lys	CCA Pro	CTC Leu	TTC Phe	TTC Phe	720	ACT Thr	ATC Ile	AAC Asn	CTC Leu	ATC Ile	ATC Ile	CCC Pro	TGC Cys	GTA Val	CTC Leu	750	
ATC Ile 251	ACC Thr	TCG Ser	CTG Leu	GCC Ala	ATC Ile	CTG Leu	GTC Val	TTC Phe	TAC Tyr	CTG Leu	CCC Pro	TCA Ser	GAC Asp	TGT Cys	810	GGT Gly	GAA Glu	AAG Lys	ATG Met	ACA Thr	CTT Leu	TGT Cys	ATT Ile	TCT Ser	GTG Val		
CTG Leu 276	CTA Leu	GCA Ala	CTC Leu	ACG Leu	GTG Val	TTC Phe	CTG Leu	CTG Leu	CTC Leu	ATC Ile	ICC Ser	AAG Lys	AAG Lys	ATT Ile	870	CCT Pro	CCC Pro	ACC Thr	TCC Ser	CTC Leu	GAT Asp	GTA Pro	CCG Leu	CTG Val	900		
GGC Gly 301	AAG Lys	TAC Tyr	CTC Leu	ATG Met	TTT Phe	ACC Thr	ATG Met	GTG Val	CTA Leu	GTC Val	ACC Thr	TTC Phe	TCC Ser	ATC Ile	930	CTA Leu	GTC Val	ACC Thr	GTG Val	TGT Cys	GTG Val	CTC Leu	AAT Asn	GTG Val	CAC His		
CAC His 326	CGC Arg	TCG Ser	CCT Pro	ACC Thr	ACG Thr	CAC His	ACC Thr	ATG Met	GCC Ala	CCC Pro	TGG Trp	GTC Val	AAG Lys	GTG Val	1020	TTC Phe	CTG Leu	GAG Glu	AAG Lys	CTG Leu	CCC Pro	ACC Thr	CTG Leu	CTC Leu	1050		
TTC Phe 351	CTG Leu	CAG Gln	CAG Gln	CCA Pro	CGC Arg	CAC His	CAC Arg	TGT Cys	GCA Ala	CGT Gln	CAG Arg	CGT Arg	CTG Leu	CTG Arg	1080	TTG Leu	AGG Arg	AGG Arg	CGC Arg	CGA Arg	GAG Glu	CGT Arg	GAG Glu	GAG Glu	GGC Gly		

FIG. 7B-2

1140 GAG GCG GTT TTC TTC CGT GAA GGT CCT GCG GCT GAC CCA TGT ACC TGC TTT GTG AAC CCT GCA TCA GTG CAG GGC 1200
 Glu Ala Val Phe Phe Arg Glu Gly Pro Ala Ala Asp Pro Cys Thr Cys Phe Val Asn Pro Ala Ser Val Gln Gly
 376
 1230 TTG GCT GGG GCT TTC CGA GCT GAG CCC ACT GCA GCC GGC CCG GGG CGC TCT GTG GGG CCA TGC AGC TGT GGC CTC
 Leu Ala Gly Ala Phe Arg Ala Glu Pro Thr Ala Ala Gly Pro Gly Arg Ser Val Gly Pro Cys Ser Cys Gly Leu
 401
 1290 CCG GAA GCA GTG GAT GGC GTA CGC TTC ATT GCG GAC CAC ATG CGA AGT GAG GAT GAT GAC CAG AGT GTG AGG GAG 1350
 Arg Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Gln Ser Val Arg Glu
 426
 1380 GAC TGG AAA TAC GTT GCC ATG GTG ATC GAC CGC CTG TTC CTG TGG ATC TTT GTG TTT TGT TGT TTT GGG ACC
 Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Phe Val Phe Val Cys Val Phe Gly Thr
 451
 1440 GTC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACT GCC ACT ACC TTC CTC CAC CCT GAC CAC TCA GCT CCC 1500
 Val Gly Met Phe Leu Leu Pro Leu Phe Phe Thr Ala Thr Thr Phe Leu His Pro Asp His Ser Ala Pro
 476
 1596 AGC TCC AAG TGAGGTCATTCATTTTGCAGCTCCTCACCCCGTGACCCCTGCGGTTTCAGTACTGGGTGCAAGATGGATCTCTCCCCACTCCACTGA
 Ser Ser Lys
 501
 1695 AGCCTGCTTCACACCTCCGTTACACACATAGTCTCCAGCCTGGAGGCTGGACCCGCTGCCTTGTGGTGGAGCCTTCTCCTTTCCCTCTGAGCTCGTTCA
 1794
 GGCAGGAGTGCCAAATGGTGGGGGCCACCGGCTGGTAAGTAGAGGCCAGAGATCACAGAGCCACCTACCCCGATGAGGTGCTGGAGAGAGGCCGCCAAGAAAG
 1893
 AGACAGAGTTATCTGTGACCTCCAAGTCATCGGAGAGGAGGAGGTAGGATAAGGGGCTCAGACTCTGGCAGAGTGGGGCTAGTACTTGGCGCCCAACCA
 1992
 CTTAAGTGAGCGACACTGGTCTGGGAGGACTCGAAGTGTGGGGAGCTCTCTTGGGAGCTCGGTCTCCACCCCTGTACCTCAGAGGGGCTCCAGACCCCGG
 2017
 GCTTCAGGTTCCCTTCTGCCAGTGC.....3'

FIG.7B-3

FIG. 8



FIG.9A

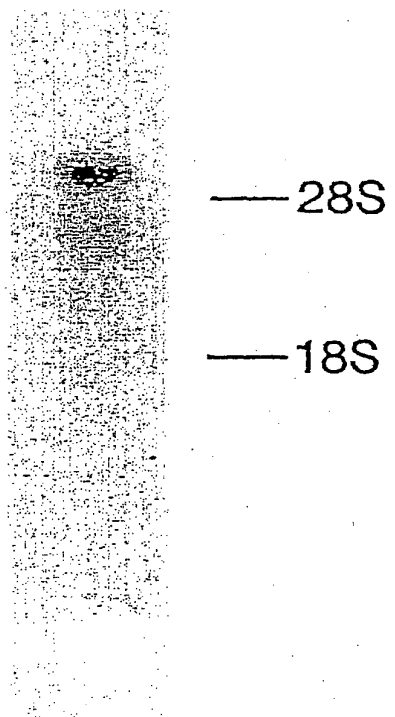


FIG.9B

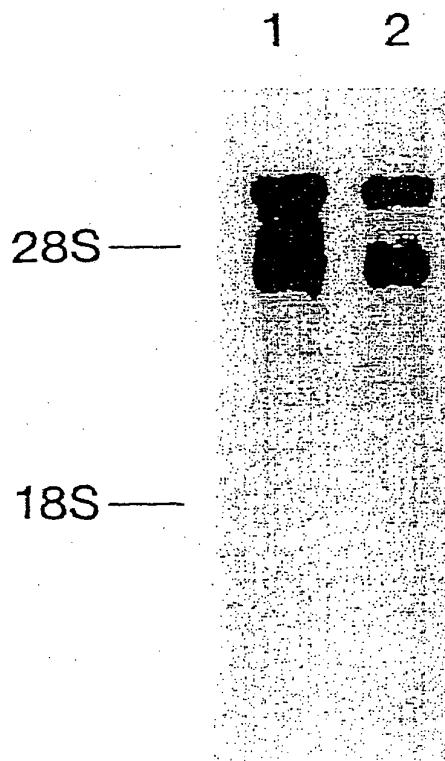


FIG. 10A
ANTISENSE

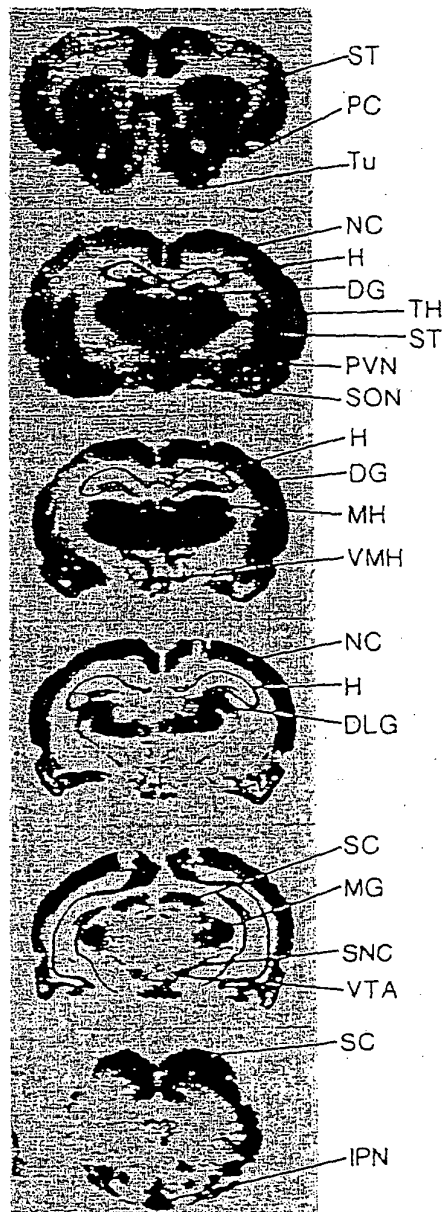
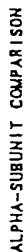


FIG. 10B
SENSE



[illegible][illegible][illegible][illegible]

ALPHA 1
 ALPHA 2
 ALPHA 3
 ALPHA 4

RSLSVOHVPSSOEAAEDGIRCRSRSIQYCVSQDGAASLADSKPTSSPTSLKARPSQLPVSDQASCKCTCKEPSVSPVTVLKAGGTAKPPQHLPLSL
 SPLIKHDEVKSRILEGKTYQETWISD
 SLSALSDIEIKKAIQSIQKIFQENHQAQ
 DALTRQVEGVQIADHLKAE
 AMPHIPATHIC HELIX
 CYTOPLASMIC REGION

ALPHA 1 QESNNALEENKQWGM. HFCGVNGLRLLTAVNAGRLIELHQQZ
ALPHA 3 NVAXE IOOQANTANU. IIRFVWVILRILHAGLRLQPLMARDDY
ALPHA 4 DTDFSVKEDPKYKQ. RIRFPMWIIIPULLLVGLRPPWLXGMI

NEVRRAVE SPANNING IV

FIG. 11

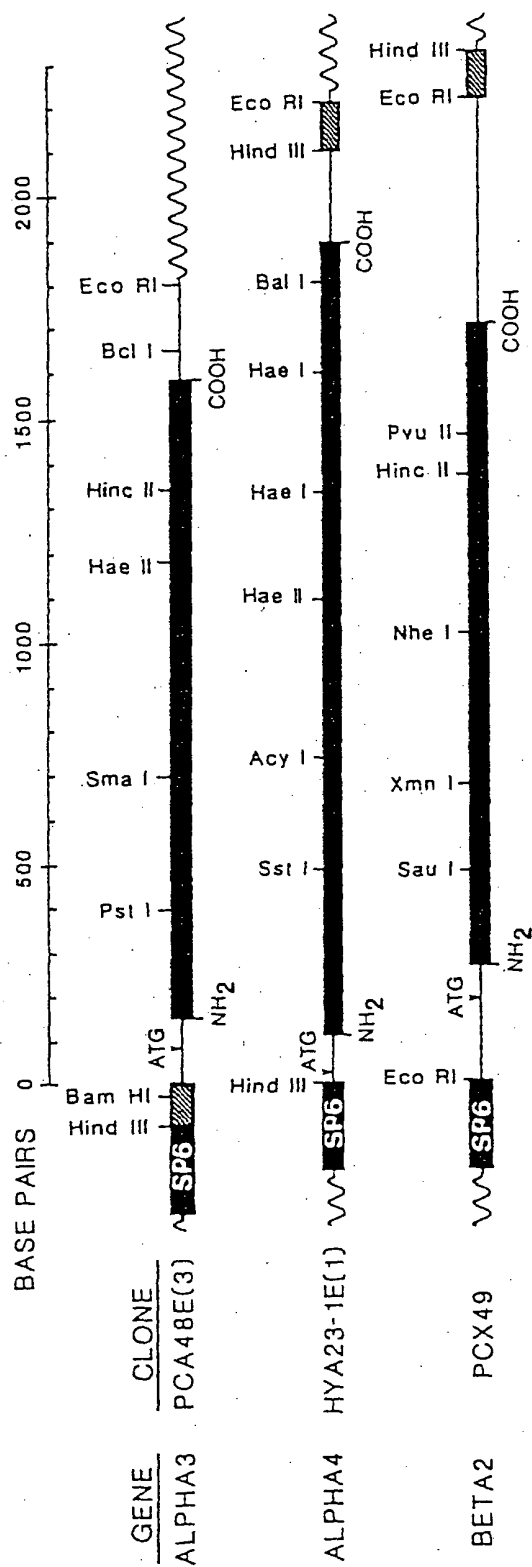


FIG.12

mRNAs injected	Responses to Acetylcholine (ACh)	Responses to Nicotine (Nic)
----------------	----------------------------------	-----------------------------

FIG.13A alpha3
 + beta2

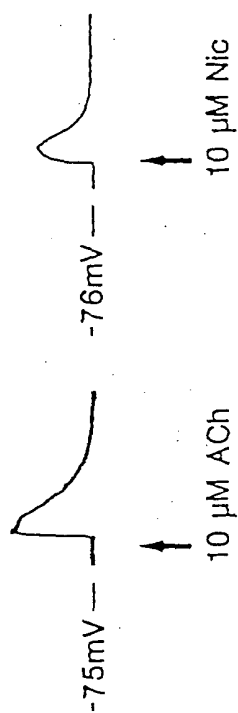


FIG.13B alpha4
 + beta2

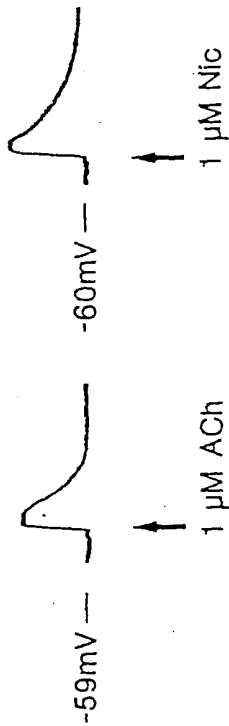
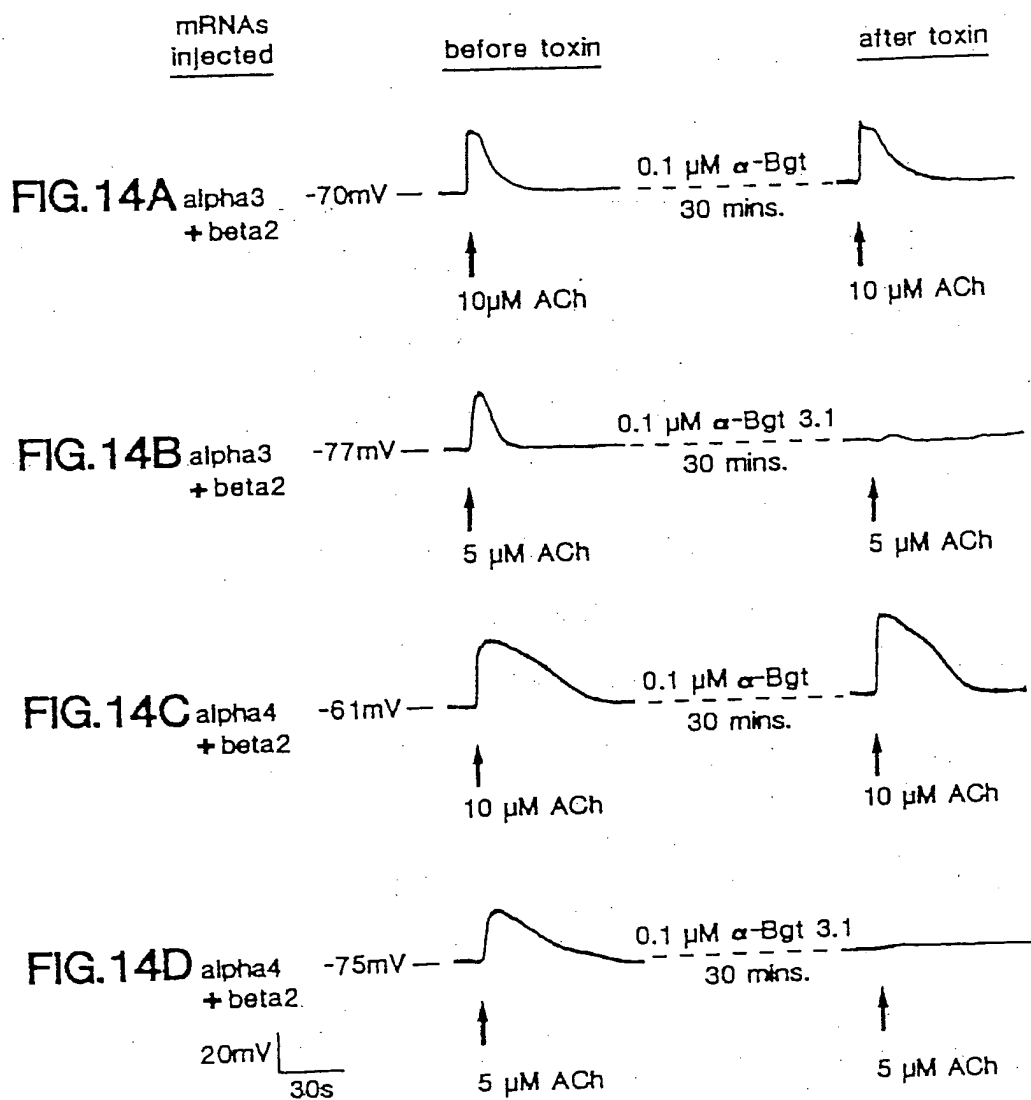


FIG.13C alpha4





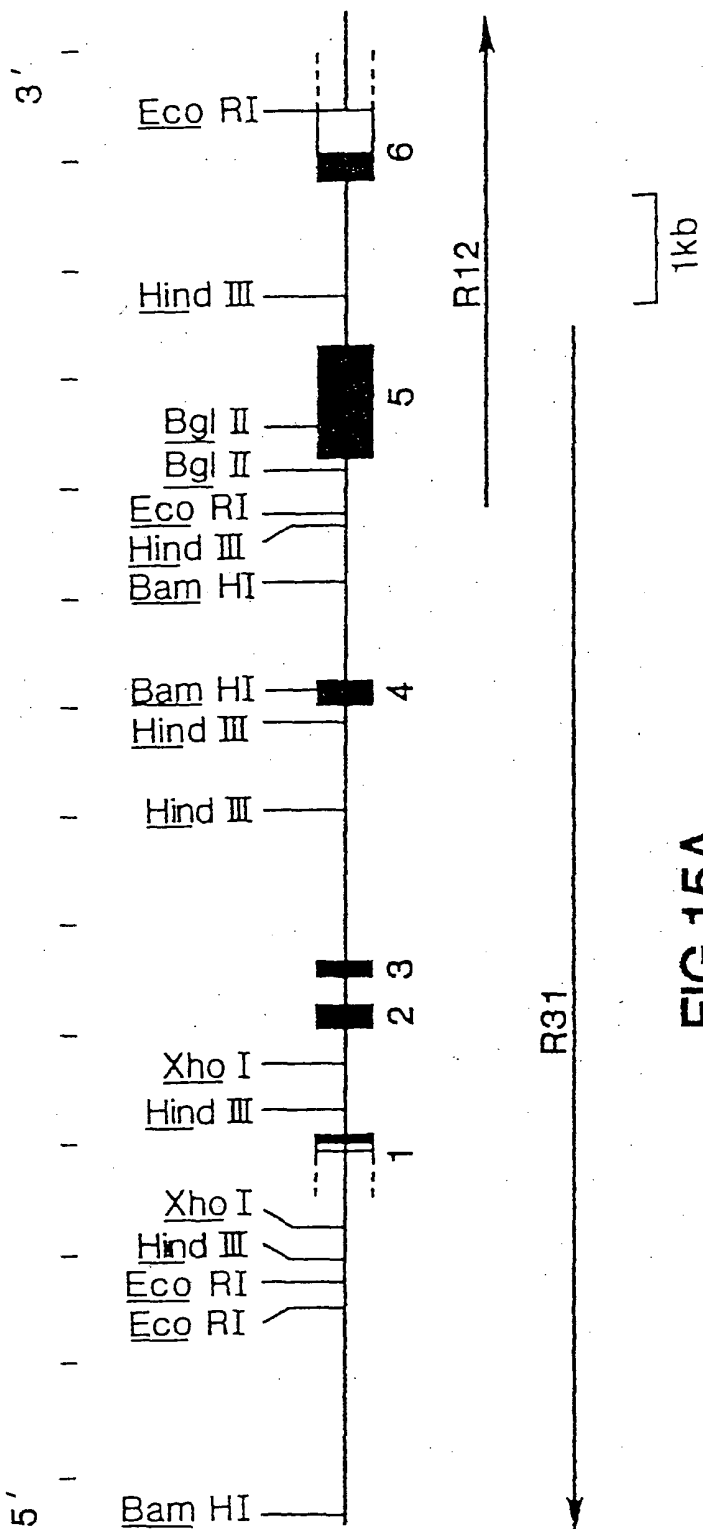


FIG.15A

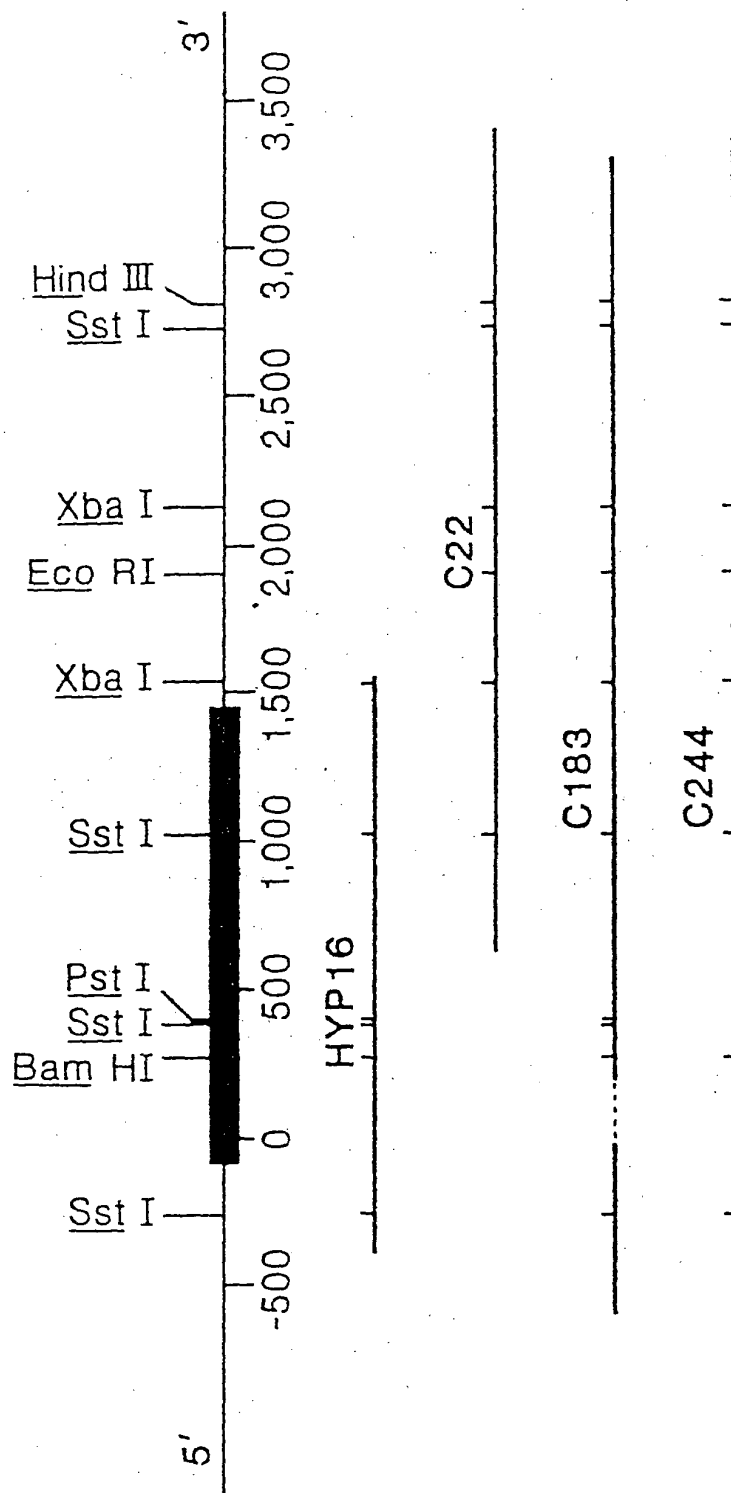
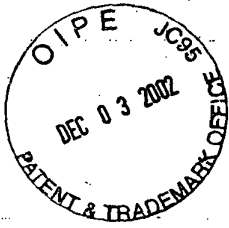
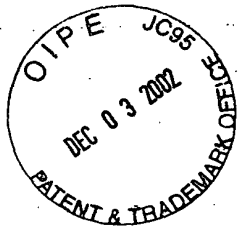


FIG.15B



5'.....ACTGAGCATTC
-360 TGTGAACTCGGATCACCTATCTCCAGGAAGCTAGCCTGAATCCCTCATCCCAACAGTGCCTCCCAACCTTGCAAGTTCTGTGTGGGCAACCATGAGCTGAAGCAACTGAGCTCTG
-330
-270
TTCTGCACCTGTGCACGTGCTCCGAGGAGCCCTCGTCAAGCCACCCAGGCTCTCCAGCGGTGGTTCTCTGCAATCCCTTGAGGGGCGCTGTCTTCTATGACAATTGCAGAGAGACAGT
-240
-210
-180
-150
GCCTCAAGAAGCCAGCTCTTGGTAGTCCAGGGAACAGGACCCCTCTGAGCC ATG ACC CTT TCC CAT TCT GCT CTC CAG TTC TGG ACA CAT CTT TAT CTC
-120
-90
-60
-30
TGG TGT CTC CTT CTG GTG CCA GCA G gtaagt.....tatccacag TG TTG ACC CAG CAA GGC TCA CAC ACC CAT GCT GAG GAC CGC CTG TTC
Trp Cys Leu Leu Val Pro Ala V al Leu Thr Gln Gln Gly Ser His Thr His Ala Glu Asp Arg Leu Phe
-10
AAA CAC CTG TTT GGA GGC TAC AAT CGC TGG GCA CGG CCA GTG CCC AAC ACT TCT GAT GTG GTC ATC GTG CGC TTT GGA TTA TCC ATT GCT
Lys His Leu Phe Gly Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr Ser Asp Val Ile Val Arg Phe Gly Leu Ser Ile Ala
60
CAG CTC ATA GAT GTG gtgggc.....gctacaacag GAT GAG AAG AAT CAA ATG ATG ACC ACC AAT GTC TGG CTA AAG CAG gtaaac.....
Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Thr Thr Asn Val Trp Leu Lys Gln
150
210
.....ccctaagcag GAA TGG AAT GAC TAC AAG CTG CGC TGG GAC CCG GCT GAG TTT GGC AAT GTG ACC TCC CTG CGC GTC CCT TCA GAG ATG
Glu Trp Asn Asp Tyr Lys Leu Arg Trp Asp Pro Ala Glu Phe Gly Asn Val Thr Ser Leu Arg Val Pro Ser Glu Met
70
80

FIG.15C-1



270 ATC TGG ATC CCA GAC ATT GTC CTC TAC AAC AA gtaaga.....ctcttccag T 300 GCA GAT GGG GAG TTT GCG GTG ACC CAC ATG ACC AAG
 Ile Trp Ile Pro Asp Ile Val Leu Tyr Asn As 100 n Ala Asp Gly Glu Phe Ala Val Thr His Met Thr Lys
 90
 360 GCT CAC CTC TTC TTC ACG GGC ACT GTG CAC TGG GTG CCC CCA GCC ATC TAC AAG AGC TCC TGC AGC ATC GAT GTG ACC TTC TTC CCC TTC
 Ala His Leu Phe Phe Thr Gly 120 Val His Trp Val Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val Thr Phe Phe Pro Phe
 450 GAC CAG CAG AAC TGC AAG ATG AAG TTT GGC TCC TGG ACA TAT GAC AAG GCC AAG ATC GAT CTG GAG CAG ATG GAG AGG ACA GTG GAC CTG
 Asp Gln Gln Asn Cys Lys Met 150 Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Glu Gln Met Glu Arg Thr Val Asp Leu
 540 AAG GAC TAC TGG GAG AGT GGC GAG TGG GCC ATT ATC AAT GCC ACC GGA ACC TAT AAT AAC AGT AAG AAG TAC GAC TGC TGC GCG GAG ATC TAC
 Lys Asp Tyr Trp Glu Ser Gly 180 Trp Ala Ile Ile Asn Ala Thr Gly Thr Tyr Asn Ser Lys Lys Tyr Asp Cys Cys Ala Glu Ile Tyr
 630 CCC GAT GTC ACC TAC TTT GTG ATC CGC CGG CTG CCG CTG TTC TAT ACC ATC AAT CTC ATC CCA TGC CTG CTC ATC TCC TGC CTC
 Pro Asp Val Thr Tyr Phe 210 Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu
 720 ACT GTG CTC GTG TTC TAC CTG CCT TCC GAG TGT GGA GAG AAG ATC ACG CTG TGC ATC TCG GTG CTG CTA TCT CTC ACT CTC TTC CTC CTG
 Thr Val Val Leu Val Phe Tyr Leu 240 Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu
 810 CTC ATC ACG GAG ATC ATC CCG TCC ACC TCG CTG GTC ATC CCA CTC ATC GGC GAG TAC CTG CTC TTC ACC ATG ATC TTT GTC ACC CTC TCT
 Leu Ile Thr Glu Ile Ile Pro 270 Thr Ser Leu Val Ile Pro Leu Ile Gly 280 Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser

FIG.15C-2



ATC GTT ATC ACA GTC TTC GTG CTC AAT GTA CAC CAC CGC ICC CCC AGC ACC CAC AAC ATG CCC AAC TGG GTA AGG GTA GCC CTG CTA GGC
11e Val 11e Thr Val Phe Val 300 Leu Asn Val His His Arg Ser Pro Ser Thr His Asn Met Pro Asn Trp Val Arg Val Ala 320 Leu Leu Gly
CGG GTG CCC AGG TGG CTG ATG ATG AAC CGG CCC CTG CCA CCT ATG GAG CTC CAT GGC TCC CCG GAT CTG AAG CTC AGC CCC TCA TAC CAT
Arg Val Pro Arg Trp Leu Met 330 Met Asn Arg Pro Leu Pro Pro Met Glu Leu His Gly Ser Pro Asp Leu Lys Leu Ser Pro Ser Tyr His
TGG CTA GAG ACT AAC ATG GAT GCT GGA GAA AGG GAG GAG ACA GAG GAA GAG GAA GAA GAT GAA AAC ATA TGT GTG TGT GCA GGC
Trp Leu Glu Thr Asn Met Asp 360 Gly Glu Arg Glu Glu Thr Glu Glu Glu Glu Glu Asp Glu Asn Ile Cys Val 380 Cys Ala Gly
CTT CCA GAC TCT TCG ATG GGT GTC CTC TAT GGC CAT GGC GGC CTG CAT CTG AGA GCC ATG GAG CCT GAG ACC AAG ACT CCA TCC CAG GCT
Leu Pro Asp Ser Ser Met Gly Val 390 Leu Tyr Gly His Gly Glu Leu His Leu Arg Ala Met Glu Pro Glu Thr Lys Thr Pro Ser Gln Ala
AGC GAG ATT CTG CTG TCA CCT CAA ATA CAG AAA GCA CTA GAA GGT GTA CAC TAC ATT GCT GAC CGT CTG AGG TCT GAG GAT GCT GAC TCT
Ser Glu Ile Leu Leu Ser Pro Gln 420 Ile Gln Lys Ala Leu Glu Gly Tyr Val 430 Tyr Ile Ala Asp Arg Leu Arg Ser Glu Asp Ala Asp Ser
TCG gtgagt.....ctaacttcag GTG AAG GAA GAC TGG AAG TAT GTG GCC ATG GTG GTA GAC CGG ATA TTC CTC TGG CTG TTC ATT ATC
Ser Val Lys Glu Asp Trp Lys 450 Val Lys Glu Asp Trp Lys 450 Val Val Ala Met Val Val Asp Arg Ile Phe Leu Trp Leu Phe Ile 460
GTC TCG TTC CTG GGG ACC ATC GGA CTC TTC CTT CCT CCA TTC CTG GCT GGA ATG ATC TAA CTTCATGTCCTTCATGTTGGCTCCAAAGGTGGCCTTCGTA
Val Cys Phe Leu Gly Thr Ile Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met Ile 480
1500 ACTATCTTCTAGTCTCTGTGAAIGGAGCCCATCTCTAGANTACTCTTTTGAC.....3'
1530
1410
1350
1380
1470

FIG.15C-3



SIGNAL PEPTIDE

[illegible]

	MEMBRANE SPANNING I				MEMBRANE SPANNING II				MEMBRANE SPANNING III			
ALPHA1	IIIT	IRFV	IRVQ	IRVY	IIIC	IRFV	IRVQ	IRVY	IIIS	IRFV	IRVQ	IRVY
ALPHA2	IVVI	IVFV	IVIR	IVYQ	IIIC	IVFV	IVIR	IVYQ	IIIS	IVFV	IVIR	IVYQ
ALPHA3	IIIS	ISLY	IRIR	IRYQ	IIIC	ISLY	IRIR	IRYQ	IIIS	ISLY	IRIR	IRYQ
ALPHA4	IIIS	ISAF	IRIR	IRYQ	IIIC	ISAF	IRIR	IRYQ	IIIS	ISAF	IRIR	IRYQ

ALPHA1 IDTQWIMFFSTWKRPSROKQKRIFTDIDISDICKPPPMGFH
ALPHA2 LGRVDRWLWNRPLPPNUEHGGSPOLKLSPSYHWLETHNDAGEREETEEEEEEDENICVACGLPOSSMGVLYHGGLHLRAMEPETKTPSOA
ALPHA3 LNLDRVFMFTRTPTSGEDTPKTRTFYGAELSNLNCFSRADSKCKEGYCODGTGCGYCHRRVYISNFSANLTRSSSESSESVNAV
ALPHA4 LDIVYRLLFMKRPSVVKONCRRLIESMHWKMANAPRPEPVEQEGILSDICNOGLSPAPTFCNPTDIAVETOPTCRSPLEVPDLKTSEVEKASPCPSCGPPKSSSGAPMLIKA

[illegible]

ALPHA1 QESNAAEEKGGGKHHHLLGGVGLGLITLAVDAGRLIELHGOO
ALPHA2 DADSSVKEDMSKGGVRRFVNLIIIGLFLPPLFLAGLI
ALPHA3 NVAKEIQDDKSGKGGVIRFVNLIIIGLFLPPLFLAGLI
ALPHA4 DTDFSVKEDMSKGGVRRFVNLIIIGLFLPPLFLAGLI

Fig. 16

FIG.17A

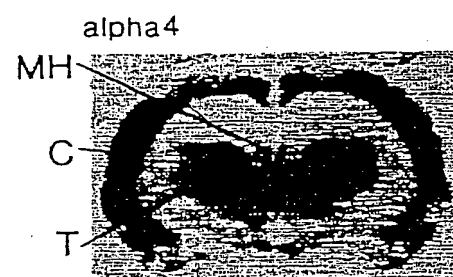
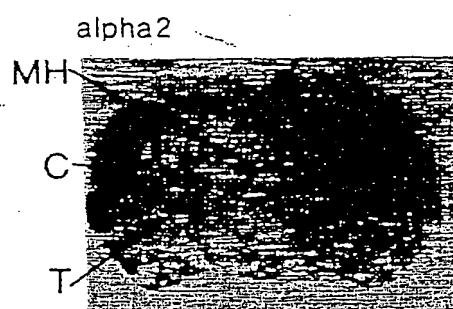
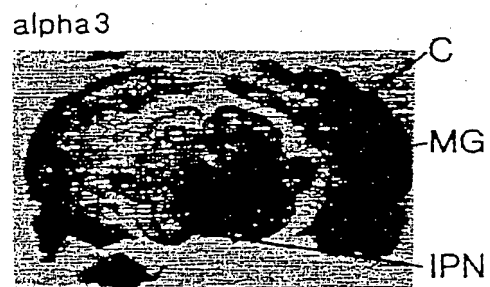
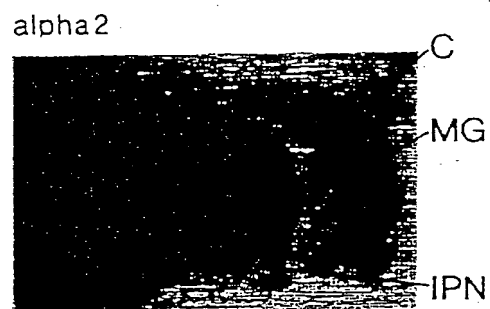


FIG.17B



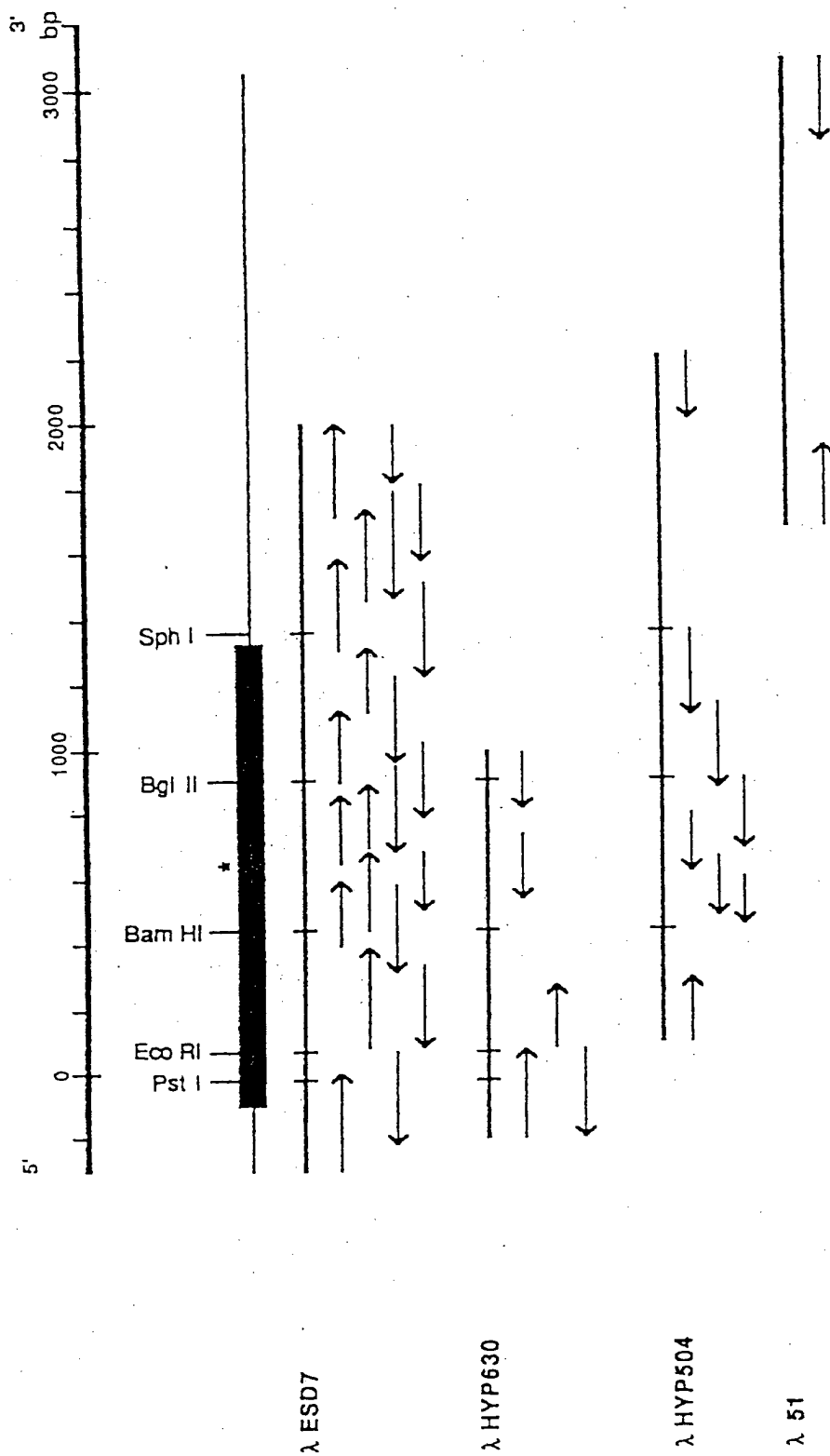


FIG. 18A

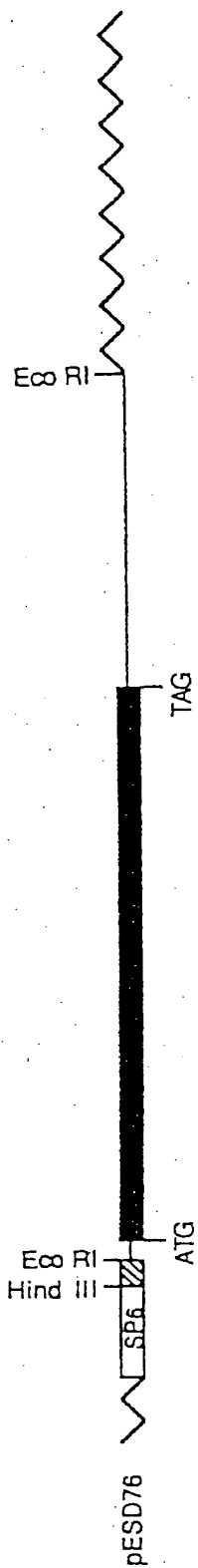
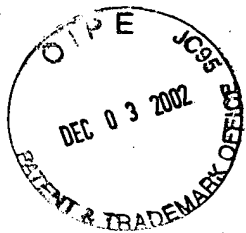


FIG.18B

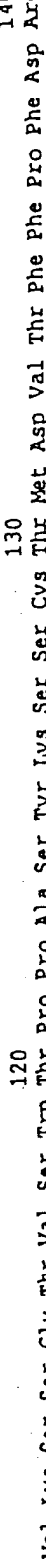


FIG. 19A

150
Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Thr Met Val Asp Leu Ile Leu Ile Asn Glu Asn Val Asp Arg Lys Asp
CAG AAC TGC TCG ATG AAG TTT GGA TCC TGG ACT TAC TAC GAC GGT ACC ATG GGT GAC CTC ATT CTA ATC AAT GAA AAC GTT GAC CGG AAA GAC
440 460 500

170
Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Lys Gly Met Lys Gly Asn Arg Arg Glu Gly Phe Tyr Ser Tyr Pro Phe Val Thr
TTT TTT GAT AAC GGA GAG TGG GAG ATA CTC AAC GCA AAG GGG ATG AAG GGC AAC AGA AGA GNA GGC TTT TAC TCC TAT CCG TTT GTT ACC
520 540 560 580 600

180
Tyr Ser Phe Val Leu Arg Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Leu Gly Leu Ser Phe Leu Thr Val Leu Val
TAC TCT TTT GTC CTG AGA CGC CTG CCC TTG TTT TAC ACG CTC TTT TTG ATA ATC CCC TGC CTG GGG TTG TCT TTT CTC ACG GTC CTG GTG
620 640 660 680

210
Phe Tyr Leu Pro Ser Asp Glu Gly Glu Lys Leu Ser Leu Ser Thr Ser Val Leu Val Ser Leu Thr Val Phe Leu Val Ile Glu Glu
TTC TAC CTA CCC TCG GAC GAA GGG GAA AAA CTC TCA TTA TCC ACC TCC GGT TTG GTC TCT TTG ACG GTG TTT CTT TTA GTG ATT GAA GAA
700 720 740 760 780

240
Ile Ile Pro Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met Ile Phe Val Thr Leu Ser Ile Ile Val Thr
ATA ATC CCG TCC TCT TCG AAG GTC ATC CCC CTC ATT GGC GAG TAC CTC CTC TTC ATT ATG ATT TTT GTC ACG CTG TCT ATT ATC GTC ACG
800 820 840 860 880

270
Val Phe Val Ile Asn Val His His Arg Ser Ser Ser Thr Tyr His Pro Met Ala Pro Trp Val Lys Arg Leu Phe Leu Gln Arg Leu Pro
GTT TTT GTA ATT AAT GTC CAC CAC ACA TCT TCC TCA ACG TAC CAT CCC ATG GCC CCC TGG GTG AAG AGG CTG TTT CTA CAA AGA CTC CCG
900 920 940 960 980

300
Arg Trp Leu Cys Met Lys Asp Pro Met Asp Arg Phe Ser Phe Pro Asp Gly Lys Glu Ser Asp Thr Ala Val Arg Gly Lys Val Ser Gly
AGA TGG CTT TGC ATG AAG GAC CCC ATG GAC CGC TTC TCT TTC CCG GAT GGA AAG GAG AGT GAT ACA GCC GTG AGG GGG AAA GTC TCA GGC
1000 1020 1040

FIG.19B



360 370 380
Lys Arg Lys Gln Thr Pro Ala Ser Asp Gln Arg Val Leu Val Ala Phe Leu Gln Lys Ala Ser Glu Ser Ile Arg Tyr Ile Ser Arg
AAA AGG AAA CAG ACT CCC GCC AGC GAT GGA GAA AGA GTT CTG CTC GCT TTC CTC GAG AAG GCC TCC GAG TCC ATC AGA TAC ATT TCG AGG
1060 1080 1100 1120 1140
390 400 410
His Val Lys Lys Glu His Phe Ile Ser Gln Val Val Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Leu Phe
CAT GTG AAA AAG GAA CAC TTC ATC ACC CAG GTA GTG CAA GAC TGG AAA TTT GTG GCT CAA GTT CTG GAC CGC ATC TTC CTG TGG CTC TTT
1160 1180 1200 1220
420 430
Leu Ile Ala Ser Val Leu Gly Ser Ile Phe Ile Pro Ala Leu Lys Met Trp Ile His Arg Phe His
CTG ATA GCT TCT GTG TTG GGT TCC ATT CTG ATT TTT ATT CCA GCC TTG AAG ATG TGG ATA CAT CGT TTC CAC TAG GAGCCACTCTCTGGACCCA
1240 1260 1280 1300 1320
TTTGAAGACATATAGACACAATCCCACTTAGGACTGACAGCGGCTGSCATGCTGACAGGAAGCAGAGCCATGCAATGTTGGTGGCTTGTCTTGTCTGGAGGCTTTCTGTG
1340 1360 1380 1400 1420 1440
ATTGAGGGCACTGAGAGAATGTGGGTTTGAGTTAGTGACATGGTGGCTGCCATTAGAGGTGTAGTTGGGCAATTTGGAGAGCTCTCCATGTTATATTGTTATGTGGGAGTTCTCTGAAC
1460 1480 1500 1520 1540 1560
TACTCCCTCTGCTCATCCCTGAAGCCACTGGGGCTATGTGGTATTTCTTAGCAGGTGTGCTGTAAGCCATTTTGACAATAGTTTTCAGGAATTCAGGAGTACAACTCTCCACACACAGG
1580 1600 1620 1640 1660 1680
TCAAATTTGCCACTTGTCAACGAGTGTCCACAAATAGGGTCATTTGAAGATGACCTTGAATGGCTATGACAGTTCCTCTAAGCCAGGTGTTACTGGAACTTTCCTCAGCTGACCTGGGAC
1700 1720 1740 1760 1780 1800
TTTTCGAATCCAGTAGGAACCTCGGGTGATTTCTAGCTTCTGTAAGGTTCCATCAAAATTAATTTACCCCAAGAAACAGCCATTCCGCTAGTAGAAGTATTTATTTCACACACATCTC
1820 1840 1860 1880 1900
TTTTTTTCCC.....3'
1930

FIG.19C



NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNITS

BETA 3	MTGFLRFLVLSATLSGSSWTLTATAGLSSVAFHEDALLRHLFOGKOKVPPVLSLSDI IKVYFGLKISQIVQVQKNEIMTNVAKDEMTDOKLRVWDEEYGGI
BETA 2	MLACMAGHNSWALFESLLWLCSGVLGTDIGERLVEHLDPSSYKLIIPATNGSELVTVOLMVSLACIISQIHEREDIMTAVWTPDEEYRRTWKREDFDNM
ALPHA 2	MTLSHSALOFWTHLYWCLLLVPVALLTOOGSHTHADRLFKH LFGGQYRWADVPVNTSOWIVFGLSIACI IDQKQKQMTITVAKDEANTYKLRNDLAEFGNV
ALPHA 3	MGVLLPPPLSLMLVLLVLLPAASASEAGHRLFOY LFGGQYRWADVPVNTSOWIVFGLSIACI IDQKQKQMTITVAKDEANTYKLRNDLAEFGNV
ALPHA 4	MEIGGPGAPPPPLLLPLLLLTGTLGPASSHITRAHAEERLLKR LFGGQYRWADVPVNTSOWIVFGLSIACI IDQKQKQMTITVAKDEANTYKLRNDLAEFGNV
	<-----SIGNAL PEPTIDE----->
BETA 3	NSIKVQSESLNLDIIPFENADRRFEGSLTKAIKVKSSGTVSMIPPAKYKSSGTVMTTFFETDRONGSWKIGSWTIDGTAVDILINEMVDRKDFDNRWEI NAKG
BETA 2	KKVRLQSKHMLIDVLYNADQAYEVFSYSNVYSDGSIEMPPAIKYKSAKIEKHFPTDQDNCITKIRMTITDTEIDILVLSKDVASLDDTPSGREWOIIALPG
ALPHA 2	TSLRVQSEMIIPDILVYNADQEFATHTKALHFFITGTVHWPPAIKYKSSGIDVTFPTDQDNCITKIRMTITDTEIDILVLSKDVASLDDTPSGREWOIIALPG
ALPHA 3	EFARVYAEKIKKPDILVYNADQFOVDDTKALKYTBVTMPPAIKYKSAKIDVTFPTDQDNCITKIRMTITDTEIDILVLSKDVASLDDTPSGREWOIIALPG
ALPHA 4	TSIRIQSELINRPDILVYNADQFAVTHLTAKHLFYDQYVQVTPPAIKYKSSGIDVTFPTDQDNCITKIRMTITDTEIDILVLSKDVASLDDTPSGREWOIIALPG
	<-----TMD 1----->
BETA 3	MKGNRR EGFYS YPFVTSFVLRRLDIFLYLFIIPGGLSEITVVFYLPDSQEGELSLTSVLVSLTIVLLVFEIINSSKVLITCEYLITIMIFVILSIV
BETA 2	RRNENPDOSTIVDIIVDFIIRKRLFYIINLIIPCVLITSALIVFYLPDSQEGELSLTSVLVSLTIVLLVFEIINSSKVLITCEYLITIMIFVILSIV
ALPHA 2	TYNSKKYDCCAEI YPDVITYFVIRRLDIFLYLFIIPGGLSEITVVFYLPDSQEGELSLTSVLVSLTIVLLVFEIINSSKVLITCEYLITIMIFVILSIV
ALPHA 3	YKHEIKYNCCAEI YODITYSLYIRRLDIFLYLFIIPGGLSEITVVFYLPDSQEGELSLTSVLVSLTIVLLVFEIINSSKVLITCEYLITIMIFVILSIV
ALPHA 4	TYNTRKYECCEAEI YPDINIAFIIRRLDIFLYLFIIPGGLSEITVVFYLPDSQEGELSLTSVLVSLTIVLLVFEIINSSKVLITCEYLITIMIFVILSIV
	<-----TMD 1----->
BETA 3	TVFVIRWVHSSSTVMPAPVVKRLFORLPRWLCHKDPMDQFSFPDGG
BETA 2	SVQVWVHSSPTIITAPVVKVVF EKLDTLLFLOOPRHQCARORLRLRROREREAGEAVFFREGPAADPCTCFVNP
ALPHA 2	TVFVIRWVHSSPTIITAPVVKVVF EKLDTLLFLOOPRHQCARORLRLRROREREAGEAVFFREGPAADPCTCFVNP
ALPHA 3	TVFVIRWVHSSPTIITAPVVKVVF EKLDTLLFLOOPRHQCARORLRLRROREREAGEAVFFREGPAADPCTCFVNP
ALPHA 4	TVFVIRWVHSSPTIITAPVVKVVF EKLDTLLFLOOPRHQCARORLRLRROREREAGEAVFFREGPAADPCTCFVNP
	<-----CYTOPLASMIC REGION----->
ALPHA 4	PLEVPDLKTSEVEKASPCPSGSCPPPKSSSGAPMLIKARLSVQHVHVPSSQEAEDGIRCSRISIOYCVSDQGAASLADSKPTSSPTSLKARPSOLPVSDOASPCCKCT
	<-----TMD 1----->
BETA 3	ESDTAVRGVSKRKOTP ASDGERVLVAFLEKASESIRYISRHVKEHFISOVVQWKEVAGQIDRIELVLIASVLSILILIPALKWVTHRFH
BETA 2	ASVOGLAGAFRAEPTAG PGRSVGPCSCGLREAVGVRFADHMRSEDDOOSVRECHWYVAVIIDDIFLSTVFVGVGTGVGMLQPLFONTYATTFELHPDHSAPSSK
ALPHA 2	YGHGGLHFRAMEPETKTP SOASEILLSPOIOKALEGVHYADRLRESDADSSVKEWNTVAVVDRILEVAIIVCFLEGTIGLEPPFLAGMI
ALPHA 3	ISNFSANLTRSSSESVN AVLSLSALSPEIKELIOSVKYIAENMKAOVNAKEIODQWYVAVIIDDIFLSTVFVGVGTGVGMLQPLFONTYATTFELHPDHSAPSSK
ALPHA 4	CKEPSVSPVTLKAGGTAKAPPOLPLSPALTRAVEGVQYADHLKAEADTDFSVKEQWYVAVIIDDIFLSTVFVGVGTGVGMLQPLFONTYATTFELHPDHSAPSSK
	<-----TMD 1----->

FIG.20

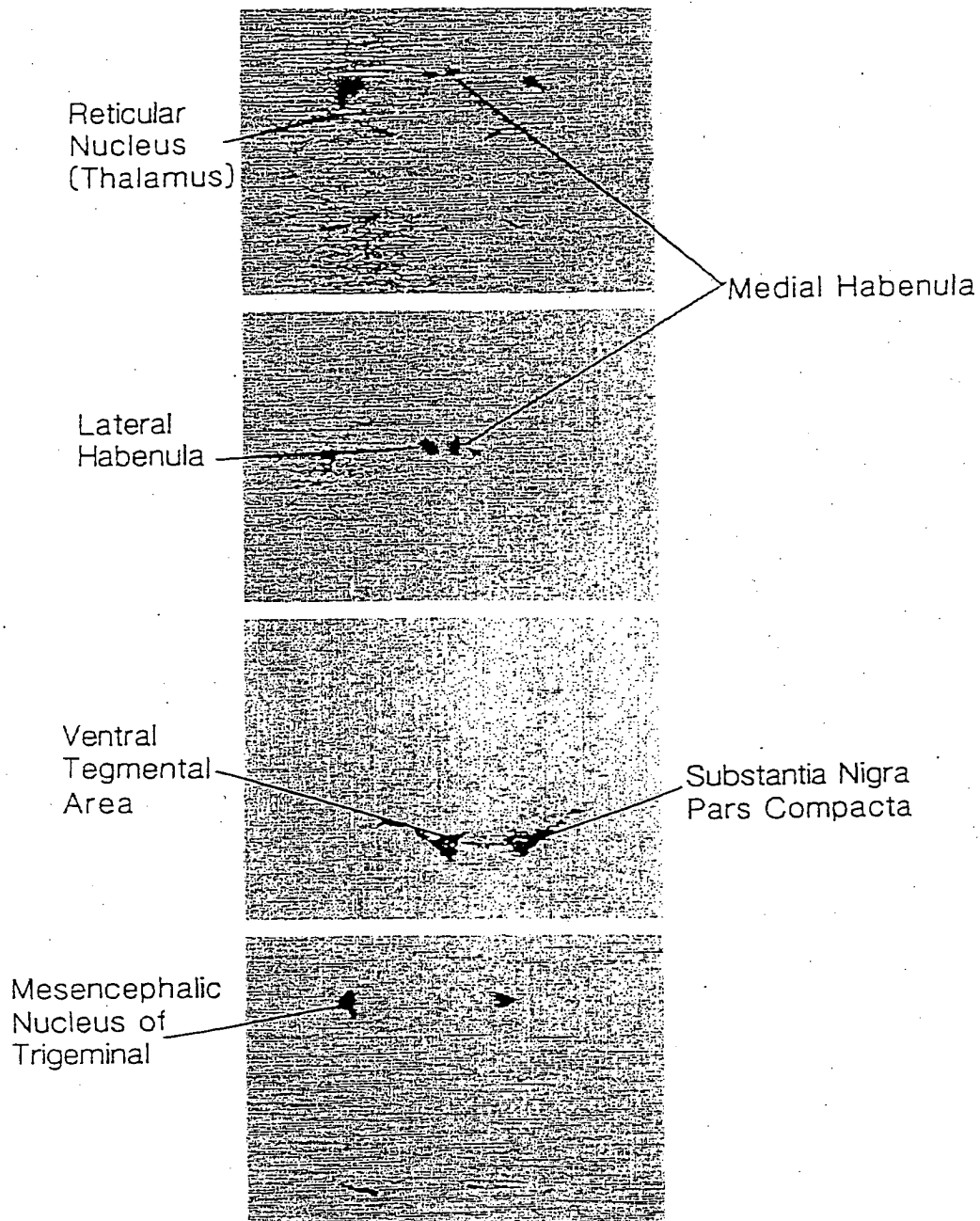


FIG.21



FIG.22

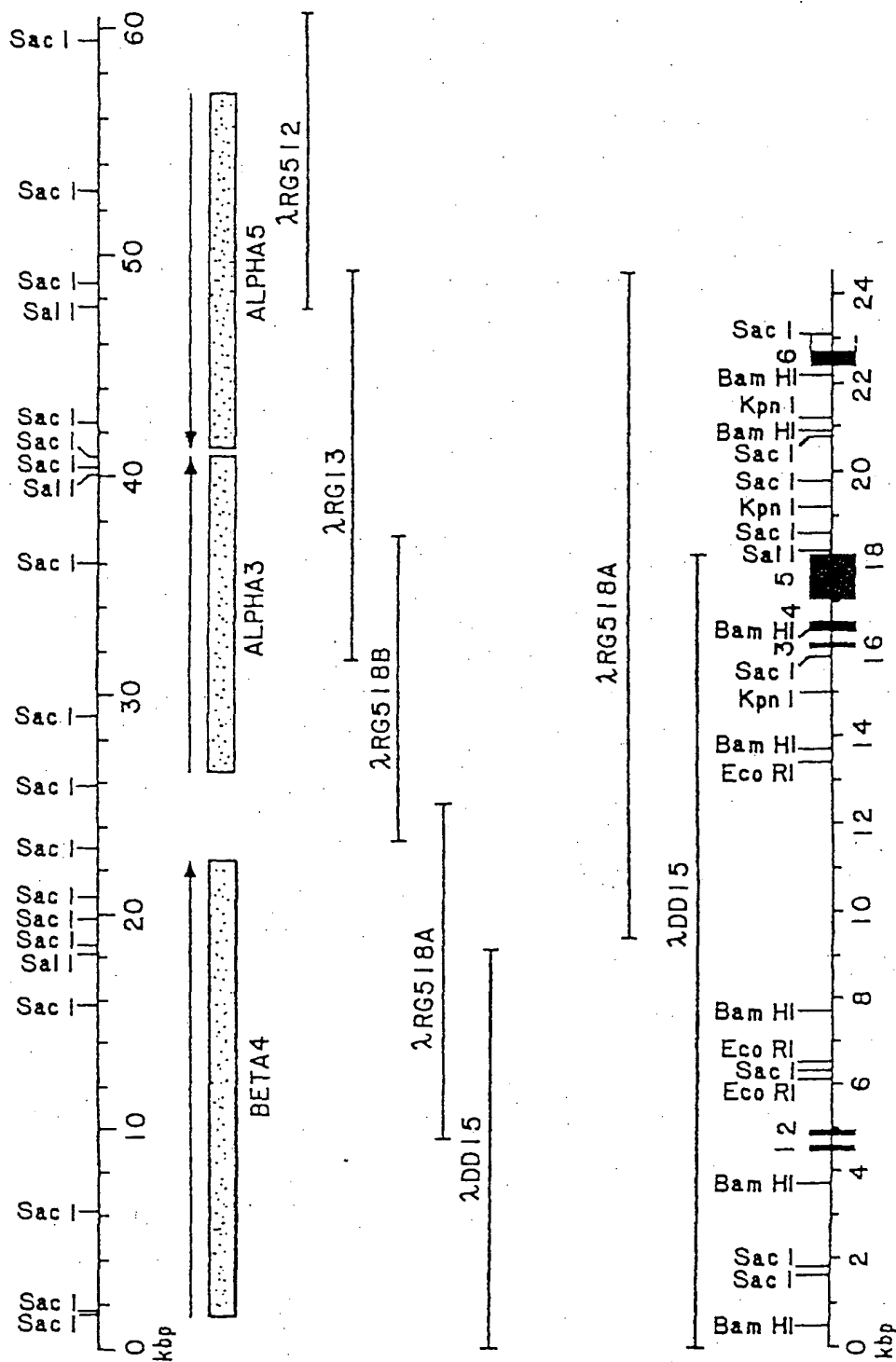


FIG.23



5'...GCCAACCGGGACAT
-120

Met Arg Gly Thr Pro Leu Leu Leu Val Ser Leu Phe Ser Leu Leu Gln Asp
-20
-10
ACGCTCACTCGCGGTTCCATTGTAGAGTACCGGCTGCCACCGGCTGGCC ATG AGG GGT ACG CCC CTG CTC CTC TCT CTG TTC TCT CTG CTT CAG GAC
-100 -80 -40 -20

-1 +1
Gly Asp Cys Arg Leu Ala Asn Ala Glu Glu Lys Leu Met Asp Asp Leu Leu Asn Lys Thr Arg Tyr Asn Asn Leu Ile Arg Pro
.....GGG GAC TGC CGC CTG GCC ACC AAC GCA GAG GAG AAG AAG CTG ATG GAT GAC CTC CTG AAC AAA ACC CGG TAC AAC AAC CTG ATC CGC CCA
1 20 40 60

Ala Thr Ser Ser Ser Gln Leu Ile Ser Ile Arg Leu Glu Leu Ser Leu Ser Gln Leu Ile Ser Val
30 40
GCC ACC AGC TCC TCT CAG CTC ATC TCC ATC CGC CTG GAG CTA TCA CTG TCC CAG CTC ATC AGT GTG
80 100 120
...ccctccccag AAT GAG
140

Arg Glu Gln Ile Met Thr Thr Ser Ile Trp Leu Lys Gln
50 60
CGA GAA CAG ATC ATG ACC ACC AGC ATC TGG CTG AAA CAG gtaagtgaact... ..cttaggaatg GAA TGG ACT GAC TAC CGC CTG GCC TGG AAC
160 180 200

Ser Ser Cys Tyr Glu Gly Val Asn Ile Leu Arg Ile Pro Ala Lys Arg Val Trp Leu Pro Asp Ile Val Leu Tyr Asn As
80 90
AGC TCC TGC TAT GAA GGG GTG AAC ATT CTG AGG ATC CCC GCA AAG CGT GTC TGG TTG CCT GAC ATC GTG TTG TAC AAC AA gtgagtgaaca...
220 240 260 280 300

n Ala Asp Gly His Tyr Glu Val Ser Val Tyr Thr Asn Val Ile Val Arg Ser Asn Gly Ser Ile Gln Trp Leu Pro Pro
100 110 120
...cctaccaccag T GCC GAT GGC ACC TAT GAG GTG TCT GTC TAC ACC AAC GTG ATT GTG CGT TCC AAC GGC AGC ATC CAG TGG CTG CCC CCT
300 320 340 360

FIG.24A

130 Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Leu Lys Phe Arg Ser Trp Thr Tyr
 GCT ATC TAC AAG AGT GCC TGC AAG ATT GAG GTG AAG CAC TTT CCC TTC GAC CAG CAG CAG AAT TTC CGC TCC TGG ACC TAT
 380 400 420 440 150
 160 Asp His Thr Glu Ile Asp Met Val Leu Lys Ser Ala Thr Ala Ile Met Asp Asp Phe Thr Pro Ser Gly Glu Trp Asp Ile Val Ala Leu
 GAC CAC ACG GAG ATT GAC ATG GTT CTT AAG TCG CCC ACG GCC ATC ATG GAT GAC TTC ACC CCC AGT GGT GAA TGG GAC ATT GTG GCC CTC
 480 500 520 540 180
 190 Pro Gly Arg Arg Thr Val Asn Pro Gln Asp Pro Ser Tyr Tyr Val Asp Val Thr Tyr Asp Phe Ile Ile Lys Arg Lys Pro Leu Phe Tyr Thr
 CCA GGA CGG AGG ACG GTG AAC CCT CAG CAG CCT CAG CCC ACG TAC GTG GAC GTG ACC TAT GAC TTC ATC ATC AAG CGC AAC GCG CTC TTC TAC ACC
 560 580 600 620 210
 220 Ile Asn Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Leu
 ATC AAT CTT ATC ATT CCT IGT GTG CTC ATC ACC TCG CTG GCT ATC CTG GTC TTC TAC CTG CCC TCC GAC TGT GGG GAG AAG ATG ACG CTC
 660 680 700 720 240
 250 Cys Ile Ser Val Leu Leu Ala Leu Thr Phe Phe Leu Leu Leu Ile Ser Lys Ile Val Pro Pro Thr Ser Leu Asp Ile Pro Leu Ile Gly
 TGC ATC TCT GTG CTG CTG GCA CTC ACG TTC TTC CTG CTG CTC ATC TCC AAG ATC GTG CCT CCC ACC TCC CTT GAC ATA CCG CTC ATT GGC
 740 760 780 800 270
 280 Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Phe Ser Ile Val Thr Val Cys Val Leu Asn Val His His Arg Ser Pro Ser Thr
 AAG TAC CTC TTG TTC ACC ATG GTG CTG GTC ACC TTT TCC ATC GTC ACC ACT GTG TGT GTG CTT AAT GTG CAC CAC GCG TCA CCC AGC ACT
 840 860 880 900 300
 310 His Thr Met Ala Ser Trp Val Lys Glu Cys Phe Leu His Lys Leu Pro Thr Phe Leu Phe Met Lys Arg Pro Gly Leu Glu Val Ser Leu
 CAC ACC ATG GCA TCC TGG GTC AAG GAG TGC TTC CTG CAC AAA CTG CCC ACC TTC CTC TTC ATG AAG CGT CCC GGT CTT GAA GTC AGC CTG
 920 940 960 980 330

FIG.24B





340 350 360
Val Arg Val Pro His Pro Ser Gln Leu His Leu Ala Thr Ser Ala Leu Gly Pro Thr Ser Pro Ser Asn Leu
3TC AGG GTC CCT CAT CCC AGC CAG CTG CAC TTT GGC ACA GCT GAT ACT GCA GCC ACC TCT GCC TTA GGC CCC ACC AGC CCA TCC AAC CTC
1020 1040 1060 1080

370 380 390
Tyr Gly Ser Ser Met Tyr Phe Val Asn Pro Val Pro Ala Ala Pro Lys Ser Ala Val Ser Ser His Thr Ala Gly Leu Pro Arg Asp Ala
TAT GGG AGT TCC ATG TAC TTT GTG AAC CCT GTC CCT GCT GCT CCT AAG TCT GCA GTC AGC TCC CAC ACA GCA GGC CTC CCC AGG GAT GCC
1100 1120 1140 1160 1180

400 410 420
Arg Leu Arg Ser Ser Gly Arg Phe Arg Glu Asp Leu Gln Glu Ala Leu Glu Gly Val Ser Phe Ile Ala Gln His Leu Glu Ser Asp Asp
CGT CTG AGG TCC TCC GGG AGG TTC CGG GAA GAT CTA CAG GAA GCA TTA GAG GGT GTC AGC TTC ATC GCC CAG CAT CTG GAG AGC GAT GAC
1200 1220 1240 1260

430 440
Arg Asp Gln Ser Val Ile Glu Asp Trp Lys Phe Val Ala Met Val Val Asp Arg Arg Leu Phe Leu Trp
CGA GAT CAA AGT gtagtcaactg... ...ttgtctgcag GTC ATC GAG GAC TGG AAG TTC GTC GCG ATG GTT GTT GAC CGC CTG TTC CTG TGG
1280 1300 1320 1340

450 460 470
Val Phe Val Phe Val Cys Ile Leu Gly Thr Met Gly Leu Phe Leu Pro Pro Leu Phe Gln Ile His Ala Pro Ser Lys Asp Ser
GTG TTC GTG TTT GTG TGT ATT CTG GGC ACC ATG GGG CTC TTC CTG CCA CCC CTT TTC CAG ATC CAC GCA CCC TCC AAG GAC TCC TAG GCT
1340 1360 1380 1400 1420

480 490 500
ACCCGCGNTGTCCTCGGNNCCGGGAAGTAGTAGATGATATAGAACGCGGTGGGAAGCAGGCGGTGTCTTNGGGCTACCCGGCCCTGTCTCGGGCCCCGGGGAAGTAGTAGATGATATGA
1420 1440 1460 1480 1500 1520

510 520
GAAAGCGGTGGGAAGCAGGCGGTGTCTTCGG...3'
1540

FIG.24C



CGTTGCTCGGCCCTCGGGGTCGGAGTTATCCGGAGGGCCGTCGGCGGGGCGATGGCGGTGCGGGGCGGCGCTGCGCTGCTCTTG
-180 -160 -140 -120 -100

Met Val Gln Leu Leu Ala Gly Arg Trp Arg Pro Thr Gly Ala Arg Arg Gly Thr Ala Gly Gly Leu Pro Glu Leu Ser Ser Ala Ala Lys
ATG GTG CAG CTG CTG GCA GGG CGG CGG ACC CGG CGG GCG GCG CGG GCG GCG TGG CCT GAA CTA TCC TCT GCT GCC AAA
-80 -60 -40 -20 -10 -1 1

His Glu Asp Ser Leu Phe Arg Asp Leu Phe Glu Asp Tyr Glu Arg Trp Val Arg Pro Val Glu His Leu Ser Asp Lys Ile Lys
CAT GAA GAC AGC TGG TTT AGG GAT TTA TTT GAA GAC TAC GAA AGG TGG GTT CGC CCT GTG GAA CAC CTG AGC GAC AAG ATA AAA ATC AAG
10 20 30 40 50 60 70 80 90

Phe Gly Leu Ala Ile Ser Gln Leu Val Asp Val Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu Trp Ile Asp
TTT GGC CTT GCG ATA TCT CAG TTA GTG GAT GTG GAT GAT GAG AAA AAC CAG CTG ATG ATG ACG GTC TGG TGG TGG CAG GAA TGG ATA GAT
100 120 140 160 180

Val Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile Lys Ile Ile Arg Val Pro Ser Asp Ser Leu Trp Ile Pro Asp Ile Val Leu
GTG AAA TTG AGA TGG AAT CCT GAC GAT TAT GGT GGG ATA AAG ATT ATA CGT GTT CCT TCG GAC AAC ACG ACG GTC TGG TGG TGG ATC CCA GAC ATC GTT TTG
200 220 240 260 280

Phe Asp Asn Ala Asp Gly Arg Phe Glu Gly Ala Ser Thr Lys Thr Val Val Val Arg Tyr Asn Gly Thr Val Thr Trp Thr Gln Pro Ala Asn
TTT GAT AAT GCA GAT GGA CGT TTT GAA GGG GCC AGC AGC AAA ACA GTT GTC AGG TAC AAC GGC ACT GTC ACG TGG ACG CAA CCA GCA AAC
300 320 340 360 380

Tyr Lys Ser Ser Cys Thr Ile Asp Val Thr Phe Phe Pro Phe Asp Leu Gln Asn Cys Ser Met Lys Phe Phe Gly Ser Trp Thr Tyr Asp Gly
TAC AAA AGT TCT TGC ACC ATC GAC GTT ACC TTT TTC CCG TTT GAT CTC CAA AAT TGT TCC ATG AAA TTC GGC TCG TGG ACA TAC GAT GGA
400 420 440 460 480

Ser Gln Val Asp Ile Ile Leu Glu Asp Gln Asp Val Asp Arg Thr Asp Phe Phe Asn Gly Glu Trp Glu Ile Met Ser Ala Met Gly
TCC CAG GTT GAT ATA ATC CTA GAG GAC CAA GAT GTC GAC AGA ACA GAC TTT TTC GAC AAT GGA GAG TGG GAA ATC ATG AGC GCG ATG GGG
500 520 540 560 580 600 620

Ser Lys Gly Asn Arg Thr Asp Ser Cys Cys Trp Tyr Trp Ile Thr Tyr Ser Phe Val Ile Lys Arg Leu Pro Leu Phe Tyr Thr Leu
AGC AAG GGG AAC CCG ACG GAC AGC TGC TGC TGC TAC CCC TAC ATC ATC ATC TAC TCC TTT GTG ATT AAG CCG CTG CCT CTC TTC ACC TTG
640 660 680 700 720 740 760 780 800

FIG.25A

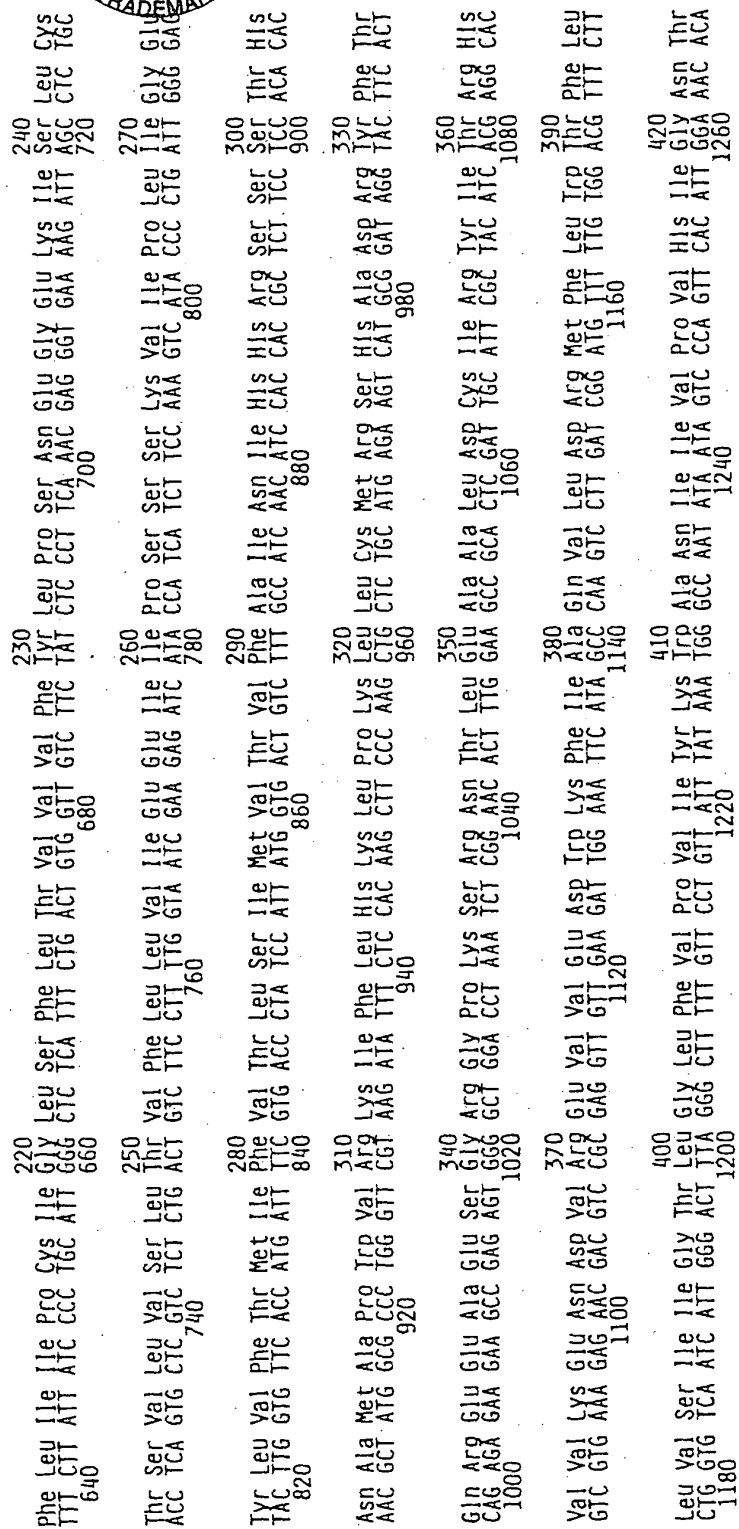


FIG. 25B



Ile Lys .
ATT AAG TGA AACCAAGAAATTACCTGTGGATTAGTAGCAGTCATGCAGCTCTTAGGACATGATGCTGTTATGGAATGTGAAGGTAGTTACAAATTTGACATAGGCTATAACA
1280 1300 1320 1340 1360 1380
GATTAGCAATTTCTAACATTGGCTTAATGTTGTCCATTAGAACTGCAGTAATAACCTCAAAATAGCAACAACACACATTGTCTGCTGCCTAGTGAAGGCTAGCATCTGCATCCCTGGCAA
1400 1420 1440 1460 1480 1500
ACCTACCAAATTTGCAACCAATGATGAAGGCCATCCTTGGAGTGCTGGAAACTCAACTGATTTTGAAGACTATTTTAAACTCCCCCAAAATTTAGTAGGAACATATATATGTGTGGTT
1520 1540 1560 1580 1600 1620
TTGAATTTTCAGAAATGGGTCTTTGGGTCTTGTTAAATTGTCTGGGCTAGCACAAAACCTCCTGAGTAGCTGGGACCATGGGTGTGCTCCACTTTGGCCCTGTTCTGTATTTCACAGATATA
1640 1660 1680 1700 1720
AAATACATCATTTTATAGGAGGTAGGCCCATTAAGTTGGTTTAAATAACTTAATGTCAAGTTAGGTTTAAATTAACCTTAATGTGAGCTAAATGTTCTATTGCTGTGAAGAGACATC
1760 1780 1800 1820 1840
ATGACCATCAACTCTTATAAAGAAACAACTTTCATCAGTGTGCTGGCTTACAGTTTGTGAGGTTTAGCCAAATATATCACAGTGAAGCATGATAGCATCCAGGTAGACATAATGCTGGATCC
1880 1900 1920 1940 1960
AGGAGTTCTCTACATCTGGATCAGCAGGCAGGAGAGAGAGAGCCACTGGACCTTGAGCATCTGAACCTCAAGGCCACCTCCAGGTGACACACACTTCCCCCAACAAGGCC
2000 2020 2040 2060 2080
ACACCTCCTAATAGTGCCACTTGTGGTGATCAAGCATTCAGTCTATGGGTCTACGAGAGCCATTCCCTATTCAAAACCACACACTTAATAGGATGCTATTCTTTACTGACATTTTAAATAAG
2100 2120 2140 2160 2180 2200
CGACAAATGGTAAC TAGAAACATCGTAGGCCACCTTACTCTTTTATGTTAATGTTATGTTGGCTTTTATATTAACTAGTTTACAGGCTATCTGAAACAACTGTAACAGGCAACTCCTG
2220 2240 2260 2280 2300 2320
CAGACACATTTCTTGTAAATGACTTTTAAATCCCTGCAGTGGCATGTTCTTGGTAAATGACTTCAGTCTCCTCGTCCACACTCTCCGGTTAGTAGAGCCATTTATGTATCATCGGCTATCCCTG
2340 2360 2380 2400 2420 2440
ATTTGAGAGCAACTGTGCAGTTGCACAGGTTCCACCTCAAAATGGGATGCCATGACTCTGTCTGGATAATTTCTGTGGAAACCACTTCTGAGCTGGATACGGTGCCTCATACCTGTCA
2460 2480 2500 2520 2540 2560
TGTCTACTTTTCAGGAGGAGAGGAGGGAATTGCTGTGAGTTGTTGGTACGCTGGTTACATATGAGAGCCCTGTCTCAGAAACCAACCAAAACCTTCCCTGTGTGAGTTGATATAAG
2580 2600 2620 2640 2660 2680
CACACTGTCTATATCCGAAATGGGGATCCTCTAGAGTCGACCTCGAGGCATGCAAGCTTGGCGTAATCATGGTTCATAGCTGTTTCCGTGTGAATTTGTTATCCG
2700 2720 2740 2760 2780

FIG.25C



BETA2 MLACHAGHSNMAFSLMLCSGVLGTDTEERLVEHLLDPSRYNKLIRPATNGSELVTQVMVSLAQIISVHEREQIMTTNVMLTQEMEDYRLTWKPEDFDMK
BETA3 HTGFLRVFLVLSATLSGSHVTLTATAGLSSVAEHEDALLRHLFOGYQKWVRVNLSSDIKIVYFGLKISQLVDDVDEKXQLMTTNVWLKQEMTDQKLRMNPPEYGGIN
BETA4 MRGTPLLVLSFSLQDQDCRLANAEKLMDDLLNKTRYNNLIRPATSSQLISIRLELSQLISVNEREQIMTTISWLKQEMTDYRLAMNSSCYEGVN

— SIGNAL PEPTIDE —

BETA2 KVLPSKHMLPDVVLNNADGMYSFYSNVSYDGSIFWLPPIYKSACKIEVKHFFPDQONCTMKFRSMTYDRTEIDLVLKSDVASLDDFTSPSGEMDIALPG
BETA3 SIKVPSSESLMLPDIVLFEENADGRFEGSLMTKAIIVKSSGTVSWTPPASYKSSCTMDVTFPPDRQNCMKFGSMTYDGTWVDLILINENVDKDFDNGEHELNAKG
BETA4 ILRIPAKRWMLPOIVLYNNADGHYEVSVYTNVIVRSNGSIQWLPPAIYKSACKIEVKHFFPDQONCTLKFRSMTYDHTIEDHVLKSATAIMODFTSPSGEMDIALPG

BETA2 RRNENPDOS TYVDITYDFIIRKKPLFYTTINLIIPCVLITSLAILVFLYLPSCGKMTLCISVLLALTIVFLLLSKIVPPTSLDVLVGYLHFTMVLVTFISVTSV
BETA3 HKGNRRREGFYSYPFVTSFVLRRPLFYTLFIIPCLGLSFLTVLFLYLPSCGKLSLSTSVLVSITVFLVIEEIIIPSSKVIPLIGEYLLFLIMIFVTLISIVTV
BETA4 RRTVNPQDP SYVDVITYDFIIRKKPLFYTTINLIIPCVLITSLAILVFLYLPSCGKMTLCISVLLALTIVFLLLSKIVPPTSLDIPLLGXKYLFLFTMVLVTFISVTV

— MSR I — — MSR II — — MSR III —

BETA2 CVLNVHHRSPST HTMAPHWKVVFLKLPITLLFLQPRHRCARQLRRLRRQREGEAVFIREGPAADPCSVGPCSCG
BETA3 FVINVHRRSSSTYHPHAPHWKRLFLQRLPRWLCHKDPHOREFSPDGKESDTAVRCVSGKXKQTPASDGERVLVAFLEK
BETA4 CVLNVHHRSPST HTMASHWKECFLHKLPTFTFMKRPGLVSLVRPHPSQLHLATADTATASALGPTSPSNLYGSSMYFVNVPVPAAPKSAVSSHTAGLPRDARLRS

BETA2 LREAVDGVRFIADHHRSEDDQSVREDWKYVAHVDRFLWIFVFCVGTGVMFLOPLFQNYTATTFLHPDHSAPSSK*
BETA3 ASESTRYISRHVKKEHFISQVQDMKXFAQVLDRIFLFLIAVGLSILIFIPALKMHIHRFH*
BETA4 SGRFREDLOALEGVSFIAQHLESDDRDQSVIEDWKYVAHVDRFLWIFVFCVILGTMGLFPLPLFQIHAPSXDS*

— MSR IV —

FIG.26



ALPHA2 HTLSHSAQPMTHLYMCLLVPAVLTOQSGSHTHAEDRLFKHLFGGYNRWARVPNPTSDVVIVRFGLSIAQLIDVDEKNQMTTNVWLKQEWNDYKLRWDPAE
ALPHA3 HGVVLLPPLSLMLVLMMLPAASASEAEHRLFYQLFEDYNEIIRPVANVSHPVIIQFEVSMQSOLVKVDEVNQIMEITNLKQIMNDYKLRWKPSPD
ALPHA4 HEIGGCPAPPFLLLLPLLLGLTGLLPASSHETRAHAEERLLKRLFGYKNSRPVGNISDVULVRGLSIAQLIDVDEKNQMTTNVWLKQEWHDYKLRWDPGD
ALPHA5 MVQLLAGRWPTGARRGTAGGLPELSSAAKHEDSLFRDLFEDYERWVRPVEHLSDKIKINFGLAISQLVDVDEKNQMTTNVWLKQEWHDYKLRWNPDD

SIGNAL PEPTIDE

ALPHA2 FGNVTLRVPSEMIWIPDVLVYNADGEFAVTHMTKAHLFTGTVHVPPAIYKSSCSIDVTFFPDQONCKMKFGSWTYDKAKIDLEQHEMTVDLKDYESGEWA
ALPHA3 YQGVFHRVPAEKIMKPOIVLYNNADGDFQVDDTKALKLYTGEVTHPPAIYKSSCKIDVTFFPDQONCKMKFGSWTYDKAKIDLVLGSMNLKDYESGEWA
ALPHA4 YENVTSIRIPSELIRWPDIVLYNNADGDFAVTHLTKAHLFDYDGRVQHTPPAIYKSSCSIDVTFFPDQONCKMKFGSWTYDKAKIDLVLSIRVDQLDYESGEWV
ALPHA5 YGGIKIIRVPSDSLWIPDIVLFDNADGRFEGAS TKTVRYNGTVMTPQANYKSSCTIDVTFFPDQONCKMKFGSWTYDGSQVDIILEDODVDRTDFFDNGEWE

**

ALPHA2 IINATGYNSKKYDCCAEIYPDVTYFVIRRLPLFYTNLIIPCLLISCLTVLVFVLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVPLIGEYLLFTMIF
ALPHA3 IIKAPGYKHEIKYNCCEIYQDITYSLYIRRLPLFYTNLIIPCLLISCLTVLVFVLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVPLIGEYLLFTMIF
ALPHA4 IVDVAGTYNTRKYECCEIYPOITYAFIIRRLPLFYTNLIIPCLLISCLTVLVFVLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVPLIGEYLLFTMIF
ALPHA5 IMSAMGSKGNRTDSCCH YPYIITYSFVIKRLPLFYTNLIIPCLLISCLTVLVFVLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVPLIGEYLLFTMIF

MSR I MSR II MSR III

ALPHA2 VTLISIVITVFLNVHHRSPSTNNMPN WVRVALLGRVPRWLMHNRPLPHELHGSPDLKLSPSYKWLTHMDAGERETEETEEEDENICVCAGLPDSSMGVLYG
ALPHA3 VTLISIVITVFLNVHRYRTPTHTMPT WVKAVFLNLLPRVMTHTPTKRTATFYGAELSNLNCFSRADSKSCKEGYPCQDGTGCGYCHRRVKISNFSANL
ALPHA4 VTLISIVITVFLNVHHRSPHTMPA WVRVFLDIVPRLFLMKRPSVVDKNCRRLLIESHMKHANAPRFPPEVGPGEILSDICNOGLSPAPTCNPTDTAVETOP
ALPHA5 VTLISIVITVFAINIHHRSSSTHNAHAPWVRKIFLKLKPLKLLCHRSADRYFTQREAEAGAGPKSRNT

ALPHA2 HGGLHLRAMEPETKTPSQA
ALPHA3 TRSSSESSEVNAV
ALPHA4 TCRSPPLEVPLDKTSEVEKASPCPSPGSCPPPKSSSGAPMLIKARSLVQHVPSSQEAEDGIRCHRSRSIQICVSDQGAASLADSKPTSSPTSLKARPSQLPVSDQ
ALPHA5

ALPHA2 SEILLSPQIQKALEGVHYIADRLRSEDADSSVKEDWKYVAMVVDRIFLWFIIVCFLGTIGLFLPPFLAGMI*
ALPHA3 SLSALSPEIKAEIQSVKYIAENMKAOQNAKEIQDDWKYVAMVVDRIFLWFIIVCFLGTIGLGTAGLFLQPLMARDDT*
ALPHA4 ASPCKCTCKEPPSPVTVLKAGGTAKAPPQHLPSPALTRAVEGVQYIADHLKAEDTFSVKEDWKYVAMVVDRIFLWFIIVCFLGTIGLGTAGLFLPPFLAGMI*
ALPHA5 LEAALDCIRYITRHHVVKENDVREVEDWKFIAQVLDORMFLWTFLLVSIIGTGLGVFPVFPINGPI*

MSR IV

FIG.27

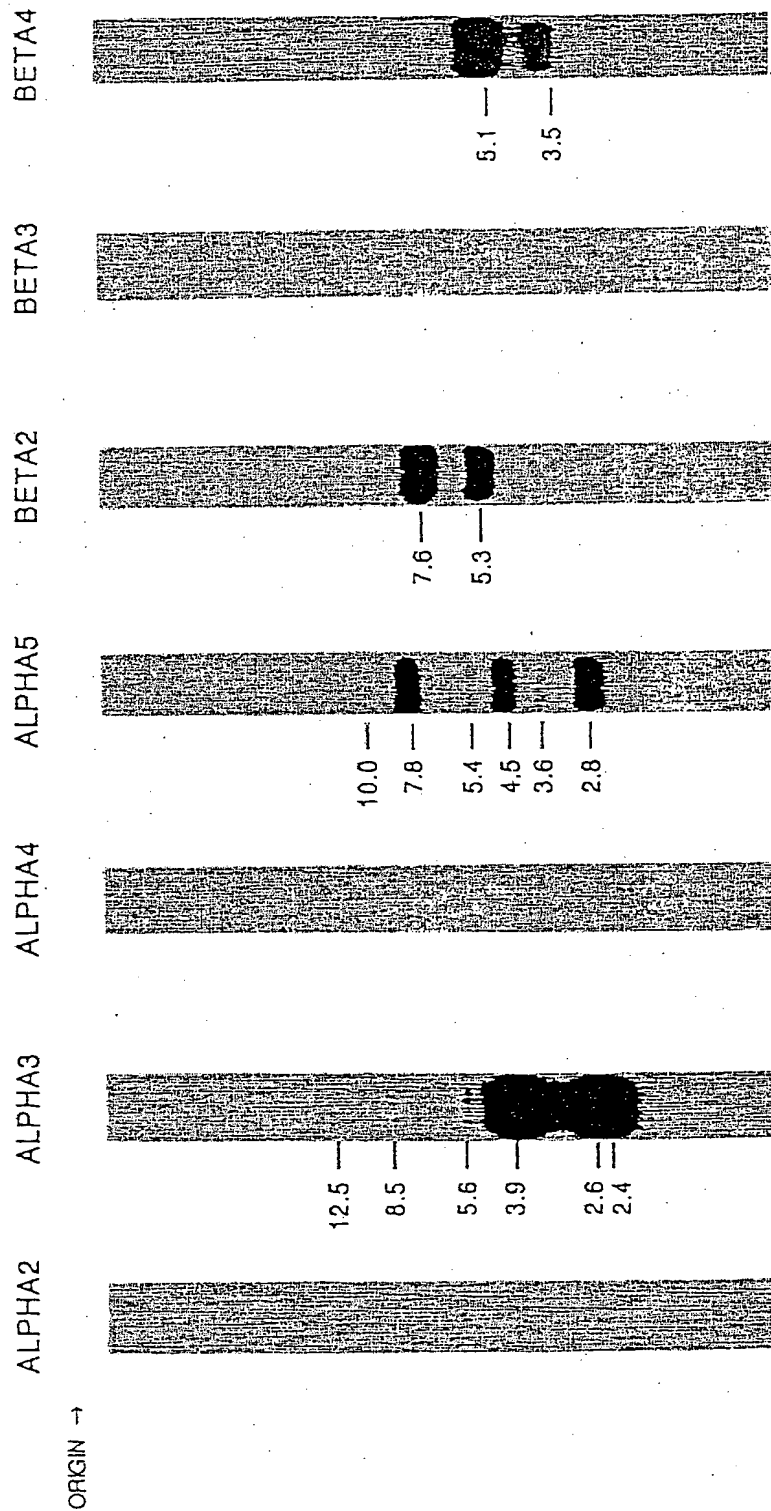


FIG.28

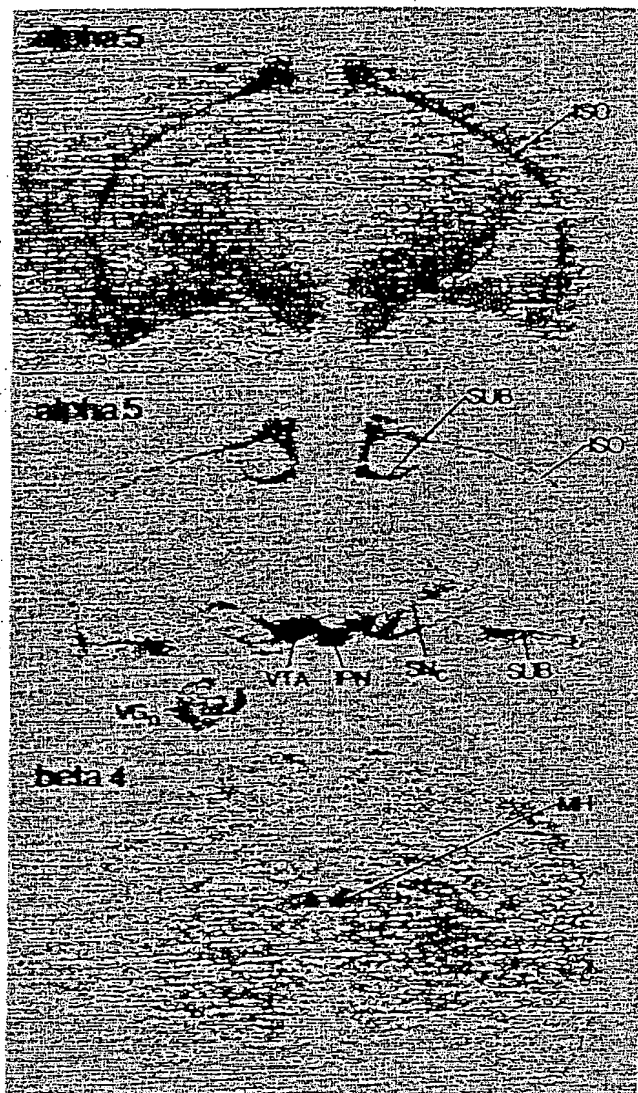


FIG.29